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(54) Title: NON-ENDOGENOUS, CONSTITUTIVELY ACTIVATED HUMAN G PROTEIN-COUPLED RECEPTORS			
(57) Abstract			
<p>The invention disclosed in this patent document relates to transmembrane receptors, more particularly to a human G protein-coupled receptor for which the endogenous ligand is unknown ("orphan GPCR receptors"), and most particularly to mutated (non-endogenous) versions of the human GPCRs for evidence of constitutive activity.</p>			

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**NON-ENDOGENOUS, CONSTITUTIVELY ACTIVATED
HUMAN G PROTEIN-COUPLED RECEPTORS**

- This patent application is a continuation-in-part of, and claims priority from, U.S. Serial Number 09/170,496, filed with the United States Patent and Trademark Office on 5 October 13, 1998. This application also claims the benefit of priority from the following provisional applications, all filed via U.S. Express Mail with the United States Patent and Trademark Office on the indicated dates: U.S. Provisional Number 60/110,060, filed November 27, 1998; U.S. Provisional Number 60/120,416, filed February 16, 1999; U.S. Provisional Number 60/121,852, filed February 26, 1999 claiming benefit of U.S. 10 Provisional Number 60/109,213, filed November 20, 1998; U.S. Provisional Number 60/123,944, filed March 12, 1999; U.S. Provisional Number 60/123,945, filed March 12, 1999; U.S. Provisional Number 60/123,948, filed March 12, 1999; U.S. Provisional Number 60/123,951, filed March 12, 1999; U.S. Provisional Number 60/123,946, filed March 12, 1999; U.S. Provisional Number 60/123,949, filed March 12, 1999; U.S. 15 Provisional Number 60/152,524, filed September 3, 1999, claiming benefit of U.S. Provisional Number 60/151,114, filed August 27, 1999 and U.S. Provisional Number 60/108,029, filed November 12, 1998; U.S. Provisional Number 60/136,436, filed May 28, 1999; U.S. Provisional Number 60/136,439, filed May 28, 1999; U.S. Provisional Number 60/136,567, filed May 28, 1999; U.S. Provisional Number 60/137,127, filed May 28, 20 1999; U.S. Provisional Number 60/137,131, filed May 28, 1999; U.S. Provisional Number

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60/141,448, filed June 29, 1999 claiming benefit of U.S. Provisional Number 60/136,437, filed May 28, 1999; U.S. Provisional Number 60/156,633, filed September 29, 1999; U.S. Provisional Number 60/156,555, filed September 29, 1999; U.S. Provisional Number 60/156,634, filed September 29, 1999; U.S. Provisional Number ____ (Arena Pharmaceuticals, Inc. docket number: CHN10-1), filed September 29, 1999; U.S. Provisional Number ____ (Arena Pharmaceuticals, Inc. docket number: RUP6-1), filed October 1, 1999; U.S. Provisional Number ____ (Arena Pharmaceuticals, Inc. docket number: RUP7-1), filed October 1, 1999; U.S. Provisional Number ____ (Arena Pharmaceuticals, Inc. docket number: CHN6-1), filed October 1, 1999; U.S. Provisional Number ____ (Arena Pharmaceuticals, Inc. docket number: RUP5-1), filed October 1, 1999; and U.S. Provisional Number ____ (Arena Pharmaceuticals, Inc. docket number: CHN9-1), filed October 1, 1999. This application is also related to co-pending U.S. Serial Number ____ (Woodcock, Washburn, Kurtz, Makiewicz & Norris, LLP docket number AREN-0050), filed on October 12, 1999 (via U.S. Express Mail) and U.S. Serial Number 09/364,425, filed on July 30, 1999, both incorporated herein by reference. This application also claims priority to U.S. Serial Number ____ (Woodcock, Washburn, Kurtz, Makiewicz & Norris, LLP docket number AREN-0054), filed on October 12, 1999 (via U.S. Express Mail), incorporated by reference herein in its entirety. Each of the foregoing applications are incorporated by reference herein in their entirety.

FIELD OF THE INVENTION

The invention disclosed in this patent document relates to transmembrane receptors, and more particularly to human G protein-coupled receptors, and specifically to

GPCRs that have been altered to establish or enhance constitutive activity of the receptor. Preferably, the altered GPCRs are used for the direct identification of candidate compounds as receptor agonists, inverse agonists or partial agonists having potential applicability as therapeutic agents.

5

BACKGROUND OF THE INVENTION

Although a number of receptor classes exist in humans, by far the most abundant and therapeutically relevant is represented by the G protein-coupled receptor (GPCR or GPCRs) class. It is estimated that there are some 100,000 genes within the human genome, and of these, approximately 2%, or 2,000 genes, are estimated to code for GPCRs. Receptors, 10 including GPCRs, for which the endogenous ligand has been identified are referred to as "known" receptors, while receptors for which the endogenous ligand has not been identified are referred to as "orphan" receptors. GPCRs represent an important area for the development of pharmaceutical products: from approximately 20 of the 100 known GPCRs, 60% of all prescription pharmaceuticals have been developed.

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GPCRs share a common structural motif. All these receptors have seven sequences of between 22 to 24 hydrophobic amino acids that form seven alpha helices, each of which spans the membrane (each span is identified by number, *i.e.*, transmembrane-1 (TM-1), transmebrane-2 (TM-2), etc.). The transmembrane helices are joined by strands of amino acids between transmembrane-2 and transmembrane-3, transmembrane-4 and transmembrane-20 5, and transmembrane-6 and transmembrane-7 on the exterior, or "extracellular" side, of the cell membrane (these are referred to as "extracellular" regions 1, 2 and 3 (EC-1, EC-2 and EC-3), respectively). The transmembrane helices are also joined by strands of amino acids between transmembrane-1 and transmembrane-2, transmembrane-3 and transmembrane-4, and

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transmembrane-5 and transmembrane-6 on the interior, or "intracellular" side, of the cell membrane (these are referred to as "intracellular" regions 1, 2 and 3 (IC-1, IC-2 and IC-3), respectively). The "carboxy" ("C") terminus of the receptor lies in the intracellular space within the cell, and the "amino" ("N") terminus of the receptor lies in the extracellular space 5 outside of the cell.

Generally, when an endogenous ligand binds with the receptor (often referred to as "activation" of the receptor), there is a change in the conformation of the intracellular region that allows for coupling between the intracellular region and an intracellular "G-protein." It has been reported that GPCRs are "promiscuous" with respect to G proteins, *i.e.*, 10 that a GPCR can interact with more than one G protein. See, Kenakin, T., 43 *Life Sciences* 1095 (1988). Although other G proteins exist, currently, Gq, Gs, Gi, Gz and Go are G proteins that have been identified. Endogenous ligand-activated GPCR coupling with the G-protein begins a signaling cascade process (referred to as "signal transduction"). Under normal conditions, signal transduction ultimately results in cellular activation or cellular inhibition. 15 It is thought that the IC-3 loop as well as the carboxy terminus of the receptor interact with the G protein.

Under physiological conditions, GPCRs exist in the cell membrane in equilibrium between two different conformations: an "inactive" state and an "active" state. A receptor in an inactive state is unable to link to the intracellular signaling transduction 20 pathway to produce a biological response. Changing the receptor conformation to the active state allows linkage to the transduction pathway (via the G-protein) and produces a biological response.

A receptor may be stabilized in an active state by an endogenous ligand or a

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compound such as a drug. Recent discoveries, including but not exclusively limited to modifications to the amino acid sequence of the receptor, provide means other than endogenous ligands or drugs to promote and stabilize the receptor in the active state conformation. These means effectively stabilize the receptor in an active state by simulating the effect of an endogenous ligand binding to the receptor. Stabilization by such ligand-independent means is termed "constitutive receptor activation."

SUMMARY OF THE INVENTION

Disclosed herein are non-endogenous versions of endogenous, human GPCRs and uses thereof.

10

BRIEF DESCRIPTION OF THE DRAWINGS

Figure 1 is a representation of 8XCRE-Luc reporter plasmid (*see, Example 4(c)3.*)

Figures 2A and 2B are graphic representations of the results of ATP and ADP binding to endogenous TDAG8 (2A) and comparisons in serum and serum free media (2B).

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Figure 3 is a graphic representation of the comparative signaling results of CMV versus the GPCR Fusion Protein H9(F236K):Gsa.

DETAILED DESCRIPTION

The scientific literature that has evolved around receptors has adopted a number of terms to refer to ligands having various effects on receptors. For clarity and consistency, the following definitions will be used throughout this patent document. To the extent that these definitions conflict with other definitions for these terms, the following definitions shall control:

AGONISTS shall mean materials (*e.g.,* ligands, candidate compounds) that

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activate the intracellular response when they bind to the receptor, or enhance GTP binding to membranes.

AMINO ACID ABBREVIATIONS used herein are set out in Table A:

TABLE A

5	ALANINE	ALA	A
	ARGININE	ARG	R
	ASPARAGINE	ASN	N
	ASPARTIC ACID	ASP	D
	CYSTEINE	CYS	C
10	GLUTAMIC ACID	GLU	E
	GLUTAMINE	GLN	Q
	GLYCINE	GLY	G
	HISTIDINE	HIS	H
	ISOLEUCINE	ILE	I
15	LEUCINE	LEU	L
	LYSINE	LYS	K
	METHIONINE	MET	M
	PHENYLALANINE	PHE	F
	PROLINE	PRO	P
20	SERINE	SER	S
	THREONINE	THR	T
	TRYPТОPHAN	TRP	W
	TYROSINE	TYR	Y
	VALINE	VAL	V

25 **PARTIAL AGONISTS** shall mean materials (*e.g.*, ligands, candidate compounds) that activate the intracellular response when they bind to the receptor to a lesser degree/extent than do agonists, or enhance GTP binding to membranes to a lesser degree/extent than do agonists.

30 **ANTAGONIST** shall mean materials (*e.g.*, ligands, candidate compounds) that competitively bind to the receptor at the same site as the agonists but which do not activate the intracellular response initiated by the active form of the receptor, and can thereby inhibit the intracellular responses by agonists or partial agonists. ANTAGONISTS do not diminish the baseline intracellular response in the absence of an agonist or partial agonist.

CANDIDATE COMPOUND shall mean a molecule (for example, and not limitation,

a chemical compound) that is amenable to a screening technique. Preferably, the phrase "candidate compound" does not include compounds which were publicly known to be compounds selected from the group consisting of inverse agonist, agonist or antagonist to a receptor, as previously determined by an indirect identification process ("indirectly identified compound"); more preferably, not including an indirectly identified compound which has previously been determined to have therapeutic efficacy in at least one mammal; and, most preferably, not including an indirectly identified compound which has previously been determined to have therapeutic utility in humans.

COMPOSITION means a material comprising at least one component; a
10 "pharmaceutical composition" is an example of a composition.

COMPOUND EFFICACY shall mean a measurement of the ability of a compound to inhibit or stimulate receptor functionality, as opposed to receptor binding affinity. Exemplary means of detecting compound efficacy are disclosed in the Example section of this patent document.

15 **CODON** shall mean a grouping of three nucleotides (or equivalents to nucleotides) which generally comprise a nucleoside (adenosine (A), guanosine (G), cytidine (C), uridine (U) and thymidine (T)) coupled to a phosphate group and which, when translated, encodes an amino acid.

CONSTITUTIVELY ACTIVATED RECEPTOR shall mean a receptor subject to
20 constitutive receptor activation. A constitutively activated receptor can be endogenous or non-endogenous.

CONSTITUTIVE RECEPTOR ACTIVATION shall mean stabilization of a receptor in the active state by means other than binding of the receptor with its endogenous

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ligand or a chemical equivalent thereof.

CONTACT or **CONTACTING** shall mean bringing at least two moieties together, whether in an in vitro system or an in vivo system.

DIRECTLY IDENTIFYING or **DIRECTLY IDENTIFIED**, in relationship to the
5 phrase "candidate compound", shall mean the screening of a candidate compound against a constitutively activated receptor, preferably a constitutively activated orphan receptor, and most preferably against a constitutively activated G protein-coupled cell surface orphan receptor, and assessing the compound efficacy of such compound. This phrase is, under no circumstances, to be interpreted or understood to be encompassed by or to encompass the
10 phrase "indirectly identifying" or "indirectly identified."

ENDOGENOUS shall mean a material that a mammal naturally produces. **ENDOGENOUS** in reference to, for example and not limitation, the term "receptor," shall mean that which is naturally produced by a mammal (for example, and not limitation, a human) or a virus. By contrast, the term **NON-ENDOGENOUS** in this context shall mean
15 that which is not naturally produced by a mammal (for example, and not limitation, a human) or a virus. For example, and not limitation, a receptor which is not constitutively active in its endogenous form, but when manipulated becomes constitutively active, is most preferably referred to herein as a "non-endogenous, constitutively activated receptor." Both terms can be utilized to describe both "in vivo" and "in vitro" systems. For example, and not limitation,
20 in a screening approach, the endogenous or non-endogenous receptor may be in reference to an in vitro screening system. As a further example and not limitation, where the genome of a mammal has been manipulated to include a non-endogenous constitutively activated receptor, screening of a candidate compound by means of an in vivo system is viable.

G PROTEIN COUPLED RECEPTOR FUSION PROTEIN and GPCR FUSION

PROTEIN, in the context of the invention disclosed herein, each mean a non-endogenous protein comprising an endogenous, constitutively activate GPCR or a non-endogenous, constitutively activated GPCR fused to at least one G protein, most preferably the alpha (α) 5 subunit of such G protein (this being the subunit that binds GTP), with the G protein preferably being of the same type as the G protein that naturally couples with endogenous orphan GPCR. For example, and not limitation, in an endogenous state, if the G protein "G α " is the predominate G protein that couples with the GPCR, a GPCR Fusion Protein based upon the specific GPCR would be a non-endogenous protein comprising the GPCR 10 fused to G α ; in some circumstances, as will be set forth below, a non-predominant G protein can be fused to the GPCR. The G protein can be fused directly to the c-terminus of the constitutively active GPCR or there may be spacers between the two.

HOST CELL shall mean a cell capable of having a Plasmid and/or Vector incorporated therein. In the case of a prokaryotic Host Cell, a Plasmid is typically replicated 15 as a autonomous molecule as the Host Cell replicates (generally, the Plasmid is thereafter isolated for introduction into a eukaryotic Host Cell); in the case of a eukaryotic Host Cell, a Plasmid is integrated into the cellular DNA of the Host Cell such that when the eukaryotic Host Cell replicates, the Plasmid replicates. Preferably, for the purposes of the invention disclosed herein, the Host Cell is eukaryotic, more preferably, mammalian, and most 20 preferably selected from the group consisting of 293, 293T and COS-7 cells.

INDIRECTLY IDENTIFYING or **INDIRECTLY IDENTIFIED** means the traditional approach to the drug discovery process involving identification of an endogenous ligand specific for an endogenous receptor, screening of candidate compounds against the

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receptor for determination of those which interfere and/or compete with the ligand-receptor interaction, and assessing the efficacy of the compound for affecting at least one second messenger pathway associated with the activated receptor.

INHIBIT or **INHIBITING**, in relationship to the term "response" shall mean that a
5 response is decreased or prevented in the presence of a compound as opposed to in the absence of the compound.

INVERSE AGONISTS shall mean materials (e.g., ligand, candidate compound) which bind to either the endogenous form of the receptor or to the constitutively activated form of the receptor, and which inhibit the baseline intracellular response initiated by the
10 active form of the receptor below the normal base level of activity which is observed in the absence of agonists or partial agonists, or decrease GTP binding to membranes. Preferably, the baseline intracellular response is inhibited in the presence of the inverse agonist by at least 30%, more preferably by at least 50%, and most preferably by at least 75%, as compared with the baseline response in the absence of the inverse agonist.

15 **KNOWN RECEPTOR** shall mean an endogenous receptor for which the endogenous ligand specific for that receptor has been identified.

LIGAND shall mean an endogenous, naturally occurring molecule specific for an endogenous, naturally occurring receptor.

MUTANT or **MUTATION** in reference to an endogenous receptor's nucleic acid
20 and/or amino acid sequence shall mean a specified change or changes to such endogenous sequences such that a mutated form of an endogenous, non-constitutively activated receptor evidences constitutive activation of the receptor. In terms of equivalents to specific sequences, a subsequent mutated form of a human receptor is considered to be equivalent to

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a first mutation of the human receptor if (a) the level of constitutive activation of the subsequent mutated form of a human receptor is substantially the same as that evidenced by the first mutation of the receptor; and (b) the percent sequence (amino acid and/or nucleic acid) homology between the subsequent mutated form of the receptor and the first mutation 5 of the receptor is at least about 80%, more preferably at least about 90% and most preferably at least 95%. Ideally, and owing to the fact that the most preferred cassettes disclosed herein for achieving constitutive activation includes a single amino acid and/or codon change between the endogenous and the non-endogenous forms of the GPCR, the percent sequence homology should be at least 98%.

10 **NON-ORPHAN RECEPTOR** shall mean an endogenous naturally occurring molecule specific for an endogenous naturally occurring ligand wherein the binding of a ligand to a receptor activates an intracellular signaling pathway.

ORPHAN RECEPTOR shall mean an endogenous receptor for which the endogenous ligand specific for that receptor has not been identified or is not known.

15 **PHARMACEUTICAL COMPOSITION** shall mean a composition comprising at least one active ingredient, whereby the composition is amenable to investigation for a specified, efficacious outcome in a mammal (for example, and not limitation, a human). Those of ordinary skill in the art will understand and appreciate the techniques appropriate for determining whether an active ingredient has a desired efficacious outcome based upon the 20 needs of the artisan.

PLASMID shall mean the combination of a Vector and cDNA. Generally, a Plasmid is introduced into a Host Cell for the purposes of replication and/or expression of the cDNA as a protein.

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STIMULATE or STIMULATING, in relationship to the term "response" shall mean that a response is increased in the presence of a compound as opposed to in the absence of the compound.

VECTOR in reference to cDNA shall mean a circular DNA capable of incorporating
5 at least one cDNA and capable of incorporation into a Host Cell.

The order of the following sections is set forth for presentational efficiency and is not intended, nor should be construed, as a limitation on the disclosure or the claims to follow.

A. Introduction

The traditional study of receptors has always proceeded from the a priori assumption
10 (historically based) that the endogenous ligand must first be identified before discovery could proceed to find antagonists and other molecules that could affect the receptor. Even in cases where an antagonist might have been known first, the search immediately extended to looking for the endogenous ligand. This mode of thinking has persisted in receptor research even after the discovery of constitutively activated receptors. What has not been heretofore recognized
15 is that it is the active state of the receptor that is most useful for discovering agonists, partial agonists, and inverse agonists of the receptor. For those diseases which result from an overly active receptor or an under-active receptor, what is desired in a therapeutic drug is a compound which acts to diminish the active state of a receptor or enhance the activity of the receptor, respectively, not necessarily a drug which is an antagonist to the endogenous ligand.
20 This is because a compound that reduces or enhances the activity of the active receptor state need not bind at the same site as the endogenous ligand. Thus, as taught by a method of this invention, any search for therapeutic compounds should start by screening compounds against the ligand-independent active state.

B. Identification of Human GPCRs

The efforts of the Human Genome project has led to the identification of a plethora of information regarding nucleic acid sequences located within the human genome; it has been the case in this endeavor that genetic sequence information has been made available without 5 an understanding or recognition as to whether or not any particular genomic sequence does or may contain open-reading frame information that translate human proteins. Several methods of identifying nucleic acid sequences within the human genome are within the purview of those having ordinary skill in the art. For example, and not limitation, a variety 10 of human GPCRs, disclosed herein, were discovered by reviewing the GenBank™ database, while other GPCRs were discovered by utilizing a nucleic acid sequence of a GPCR, previously sequenced, to conduct a BLAST™ search of the EST database. Table B, below, lists several endogenous GPCRs that we have discovered, along with a GPCR's respective homologous receptor.

TABLE B

15	Disclosed Human Orphan GPCRs	Accession Number Identified	Open Reading Frame (Base Pairs)	Per Cent Homology To Designated GPCR	Reference To Homologous GPCR (Accession No.)
20	hARE-3	AL033379	1,260 bp	52.3% LPA-R	U92642
	hARE-4	AC006087	1,119 bp	36% P2Y5	AF000546
	hARE-5	AC006255	1,104 bp	32% <i>Oryzias latipes</i>	D43633
	hGPR27 hARE-1	AA775870 AI090920	1,128 bp 999 bp	43% KIAA0001	D13626
25	hARE-2	AA359504	1,122 bp	53% GPR27	
	hPPR1	H67224	1,053 bp	39% EBI1	L31581
	hG2A	AA754702	1,113 bp	31% GPR4	L36148

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	hRUP3	AL035423	1,005 bp	30% <i>Drosophila melanogaster</i>	2133653
	hRUP4	AI307658	1,296 bp	32% pNPGPR 28% and 29 % <i>Zebrafish Ya</i> and <i>Yb</i> , respectively	NP_004876 AAC41276 and AAB94616
	hRUP5	AC005849	1,413 bp	25% DEZ 23% FMLPR	Q99788 P21462
5	hRUP6	AC005871	1,245 bp	48% GPR66	NP_006047
	hRUP7	AC007922	1,173 bp	43% H3R	AF140538
	hCHN3	EST 36581	1,113 bp	53% GPR27	
	hCHN4	AA804531	1,077 bp	32% thrombin	4503637
	hCHN6	EST 2134670	1,503 bp	36% edg-1	NP_001391
	hCHN8	EST 764455	1,029 bp	47% KIAA0001	D13626
10	hCHN9	EST 1541536	1,077 bp	41% LTB4R	NM_000752
	hCHN10	EST 1365839	1,055 bp	35% P2Y	NM_002563

Receptor homology is useful in terms of gaining an appreciation of a role of the receptors within the human body. As the patent document progresses, we will disclose techniques for mutating these receptors to establish non-endogenous, constitutively activated 15 versions of these receptors.

The techniques disclosed herein have also been applied to other human, orphan GPCRs known to the art, as will be apparent as the patent document progresses.

C. Receptor Screening

Screening candidate compounds against a non-endogenous, constitutively activated 20 version of the human GPCRs disclosed herein allows for the direct identification of candidate compounds which act at this cell surface receptor, without requiring use of the receptor's endogenous ligand. By determining areas within the body where the endogenous version of human GPCRs disclosed herein is expressed and/or over-expressed, it is possible to determine related disease/disorder states which are associated with the expression and/or over-expression

of the receptor; such an approach is disclosed in this patent document.

With respect to creation of a mutation that may evidence constitutive activation of the human GPCR disclosed herein is based upon the distance from the proline residue at which is presumed to be located within TM6 of the GPCR; this algorithmic technique is disclosed 5 in co-pending and commonly assigned patent document U.S. Serial Number 09/170,496, incorporated herein by reference. The algorithmic technique is not predicated upon traditional sequence "alignment" but rather a specified distance from the aforementioned TM6 proline residue. By mutating the amino acid residue located 16 amino acid residues from this residue (presumably located in the IC3 region of the receptor) to, most preferably, a lysine residue, 10 such activation may be obtained. Other amino acid residues may be useful in the mutation at this position to achieve this objective.

D. Disease/Disorder Identification and/or Selection

As will be set forth in greater detail below, most preferably inverse agonists to the non-endogenous, constitutively activated GPCR can be identified by the methodologies of this 15 invention. Such inverse agonists are ideal candidates as lead compounds in drug discovery programs for treating diseases related to this receptor. Because of the ability to directly identify inverse agonists to the GPCR, thereby allowing for the development of pharmaceutical compositions, a search for diseases and disorders associated with the GPCR is relevant. For example, scanning both diseased and normal tissue samples for the presence 20 of the GPCR now becomes more than an academic exercise or one which might be pursued along the path of identifying an endogenous ligand to the specific GPCR. Tissue scans can be conducted across a broad range of healthy and diseased tissues. Such tissue scans provide a preferred first step in associating a specific receptor with a disease and/or disorder. *See, for*

example, co-pending application (docket number ARE-0050) for exemplary dot-blot and RT-PCR results of several of the GPCRs disclosed herein.

Preferably, the DNA sequence of the human GPCR is used to make a probe for (a) dot-blot analysis against tissue-mRNA, and/or (b) RT-PCR identification of the expression 5 of the receptor in tissue samples. The presence of a receptor in a tissue source, or a diseased tissue, or the presence of the receptor at elevated concentrations in diseased tissue compared to a normal tissue, can be preferably utilized to identify a correlation with a treatment regimen, including but not limited to, a disease associated with that disease. Receptors can equally well be localized to regions of organs by this technique. Based on 10 the known functions of the specific tissues to which the receptor is localized, the putative functional role of the receptor can be deduced.

E. Screening of Candidate Compounds

1. Generic GPCR screening assay techniques

When a G protein receptor becomes constitutively active, it binds to a G protein (e.g., 15 Gq, Gs, Gi, Gz, Go) and stimulates the binding of GTP to the G protein. The G protein then acts as a GTPase and slowly hydrolyzes the GTP to GDP, whereby the receptor, under normal conditions, becomes deactivated. However, constitutively activated receptors continue to exchange GDP to GTP. A non-hydrolyzable analog of GTP, [³⁵S]GTP γ S, can be used to monitor enhanced binding to membranes which express constitutively activated receptors. 20 It is reported that [³⁵S]GTP γ S can be used to monitor G protein coupling to membranes in the absence and presence of ligand. An example of this monitoring, among other examples well-known and available to those in the art, was reported by Traynor and Nahorski in 1995. The preferred use of this assay system is for initial screening of candidate compounds because the

system is generically applicable to all G protein-coupled receptors regardless of the particular G protein that interacts with the intracellular domain of the receptor.

2. Specific GPCR screening assay techniques

Once candidate compounds are identified using the "generic" G protein-coupled receptor assay (*i.e.*, an assay to select compounds that are agonists, partial agonists, or inverse agonists), further screening to confirm that the compounds have interacted at the receptor site is preferred. For example, a compound identified by the "generic" assay may not bind to the receptor, but may instead merely "uncouple" the G protein from the intracellular domain.

a. *Gs, Gz and Gi.*

10 *Gs* stimulates the enzyme adenylyl cyclase. *Gi* (and *Gz* and *Go*), on the other hand, inhibit this enzyme. Adenylyl cyclase catalyzes the conversion of ATP to cAMP; thus, constitutively activated GPCRs that couple the *Gs* protein are associated with increased cellular levels of cAMP. On the other hand, constitutively activated GPCRs that couple *Gi* (or *Gz*, *Go*) protein are associated with decreased cellular levels of cAMP. *See, generally,* 15 "Indirect Mechanisms of Synaptic Transmission," Chpt. 8, From Neuron To Brain (3rd Ed.) Nichols, J.G. et al eds. Sinauer Associates, Inc. (1992). Thus, assays that detect cAMP can be utilized to determine if a candidate compound is, *e.g.*, an inverse agonist to the receptor (i.e., such a compound would decrease the levels of cAMP). A variety of approaches known in the art for measuring cAMP can be utilized; a most preferred approach relies upon the use 20 of anti-cAMP antibodies in an ELISA-based format. Another type of assay that can be utilized is a whole cell second messenger reporter system assay. Promoters on genes drive the expression of the proteins that a particular gene encodes. Cyclic AMP drives gene expression by promoting the binding of a cAMP-responsive DNA binding protein or

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transcription factor (CREB) that then binds to the promoter at specific sites called cAMP response elements and drives the expression of the gene. Reporter systems can be constructed which have a promoter containing multiple cAMP response elements before the reporter gene, e.g., β -galactosidase or luciferase. Thus, a constitutively activated Gs-linked receptor causes 5 the accumulation of cAMP that then activates the gene and expression of the reporter protein. The reporter protein such as β -galactosidase or luciferase can then be detected using standard biochemical assays (Chen et al. 1995).

b. Go and Gq.

10 Gq and Go are associated with activation of the enzyme phospholipase C, which in turn hydrolyzes the phospholipid PIP₂, releasing two intracellular messengers: diacycloglycerol (DAG) and inistol 1,4,5-triphosphate (IP₃). Increased accumulation of IP₃ is associated with activation of Gq- and Go-associated receptors. See, generally, "Indirect Mechanisms of Synaptic Transmission," Chpt. 8, From Neuron To Brain (3rd Ed.) Nichols, 15 J.G. et al eds. Sinauer Associates, Inc. (1992). Assays that detect IP₃ accumulation can be utilized to determine if a candidate compound is, e.g., an inverse agonist to a Gq- or Go-associated receptor (*i.e.*, such a compound would decrease the levels of IP₃). Gq-associated receptors can also been examined using an AP1 reporter assay in that Gq-dependent phospholipase C causes activation of genes containing AP1 elements; thus, activated Gq- 20 associated receptors will evidence an increase in the expression of such genes, whereby inverse agonists thereto will evidence a decrease in such expression, and agonists will evidence an increase in such expression. Commercially available assays for such detection are available.

3. GPCR Fusion Protein

The use of an endogenous, constitutively activate orphan GPCR or a non-endogenous, constitutively activated orphan GPCR, for use in screening of candidate compounds for the direct identification of inverse agonists, agonists and partial agonists provide an interesting 5 screening challenge in that, by definition, the receptor is active even in the absence of an endogenous ligand bound thereto. Thus, in order to differentiate between, *e.g.*, the non-endogenous receptor in the presence of a candidate compound and the non-endogenous receptor in the absence of that compound, with an aim of such a differentiation to allow for an understanding as to whether such compound may be an inverse agonist, agonist, partial 10 agonist or have no affect on such a receptor, it is preferred that an approach be utilized that can enhance such differentiation. A preferred approach is the use of a GPCR Fusion Protein.

Generally, once it is determined that a non-endogenous orphan GPCR has been constitutively activated using the assay techniques set forth above (as well as others), it is possible to determine the predominant G protein that couples with the endogenous GPCR. 15 Coupling of the G protein to the GPCR provides a signaling pathway that can be assessed. Because it is most preferred that screening take place by use of a mammalian expression system, such a system will be expected to have endogenous G protein therein. Thus, by definition, in such a system, the non-endogenous, constitutively activated orphan GPCR will continuously signal. In this regard, it is preferred that this signal be enhanced such that in the 20 presence of, *e.g.*, an inverse agonist to the receptor, it is more likely that it will be able to more readily differentiate, particularly in the context of screening, between the receptor when it is contacted with the inverse agonist.

The GPCR Fusion Protein is intended to enhance the efficacy of G protein coupling

with the non-endogenous GPCR. The GPCR Fusion Protein is preferred for screening with a non-endogenous, constitutively activated GPCR because such an approach increases the signal that is most preferably utilized in such screening techniques. This is important in facilitating a significant "signal to noise" ratio; such a significant ratio is import preferred for 5 the screening of candidate compounds as disclosed herein.

The construction of a construct useful for expression of a GPCR Fusion Protein is within the purview of those having ordinary skill in the art. Commercially available expression vectors and systems offer a variety of approaches that can fit the particular needs of an investigator. The criteria of importance for such a GPCR Fusion Protein construct is 10 that the endogenous GPCR sequence and the G protein sequence both be in-frame (preferably, the sequence for the endogenous GPCR is upstream of the G protein sequence) and that the "stop" codon of the GPCR must be deleted or replaced such that upon expression of the GPCR, the G protein can also be expressed. The GPCR can be linked directly to the G protein, or there can be spacer residues between the two (preferably, no more than about 12, 15 although this number can be readily ascertained by one of ordinary skill in the art). We have a preference (based upon convenience) of use of a spacer in that some restriction sites that are not used will, effectively, upon expression, become a spacer. Most preferably, the G protein that couples to the non-endogenous GPCR will have been identified prior to the creation of the GPCR Fusion Protein construct. Because there are only a few G proteins that have been 20 identified, it is preferred that a construct comprising the sequence of the G protein (*i.e.*, a universal G protein construct) be available for insertion of an endogenous GPCR sequence therein; this provides for efficiency in the context of large-scale screening of a variety of different endogenous GPCRs having different sequences.

As noted above, constitutively activated GPCRs that couple to Gi, Gz and Go are expected to inhibit the formation of cAMP making assays based upon these types of GPCRs challenging (*i.e.*, the cAMP signal decreases upon activation thus making the direct identification of, *e.g.*, inverse agonists (which would further decrease this signal), interesting).

- 5 As will be disclosed herein, we have ascertained that for these types of receptors, it is possible to create a GPCR Fusion Protein that is not based upon the endogenous GPCR's endogenous G protein, in an effort to establish a viable cyclase-based assay. Thus, for example, a Gz coupled receptor such as H9, a GPCR Fusion Protein can be established that utilizes a Gs fusion protein – we believe that such a fusion construct, upon expression, "drives" or "forces" 10 the non-endogenous GPCR to couple with, *e.g.*, Gs rather than the "natural" Gz protein, such that a cyclase-based assay can be established. Thus, for Gi, Gz and Go coupled receptors, we prefer that when a GPCR Fusion Protein is used and the assay is based upon detection of adenyl cyclase activity, that the fusion construct be established with Gs (or an equivalent G protein that stimulates the formation of the enzyme adenylyl cyclase).
- 15

F. Medicinal Chemistry

Generally, but not always, direct identification of candidate compounds is preferably conducted in conjunction with compounds generated via combinatorial chemistry techniques, whereby thousands of compounds are randomly prepared for such analysis. Generally, the results of such screening will be compounds having unique core structures; thereafter, these 20 compounds are preferably subjected to additional chemical modification around a preferred core structure(s) to further enhance the medicinal properties thereof. Such techniques are known to those in the art and will not be addressed in detail in this patent document.

G. Pharmaceutical compositions

Candidate compounds selected for further development can be formulated into pharmaceutical compositions using techniques well known to those in the art. Suitable pharmaceutically-acceptable carriers are available to those in the art; for example, see 5 Remington's Pharmaceutical Sciences, 16th Edition, 1980, Mack Publishing Co., (Oslo et al., eds.)

H. Other Utility

Although a preferred use of the non-endogenous versions the human GPCRs disclosed herein may be for the direct identification of candidate compounds as inverse agonists. 10 agonists or partial agonists (preferably for use as pharmaceutical agents), these versions of human GPCRs can also be utilized in research settings. For example, *in vitro* and *in vivo* systems incorporating GPCRs can be utilized to further elucidate and understand the roles these receptors play in the human condition, both normal and diseased, as well as understanding the role of constitutive activation as it applies to understanding the signaling 15 cascade. The value in non-endogenous human GPCRs is that their utility as a research tool is enhanced in that, because of their unique features, non-endogenous human GPCRs can be used to understand the role of these receptors in the human body before the endogenous ligand therefor is identified. Other uses of the disclosed receptors will become apparent to those in the art based upon, *inter alia*, a review of this patent document.

20

EXAMPLES

The following examples are presented for purposes of elucidation, and not limitation, of the present invention. While specific nucleic acid and amino acid sequences are disclosed herein, those of ordinary skill in the art are credited with the ability to make minor

modifications to these sequences while achieving the same or substantially similar results reported below. The traditional approach to application or understanding of sequence cassettes from one sequence to another (*e.g.* from rat receptor to human receptor or from human receptor A to human receptor B) is generally predicated upon sequence alignment 5 techniques whereby the sequences are aligned in an effort to determine areas of commonality. The mutational approach disclosed herein does not rely upon this approach but is instead based upon an algorithmic approach and a positional distance from a conserved proline residue located within the TM6 region of human GPCRs. Once this approach is secured, those in the art are credited with the ability to make minor modifications thereto to achieve 10 substantially the same results (*i.e.*, constitutive activation) disclosed herein. Such modified approaches are considered within the purview of this disclosure

Example 1
ENDOGENOUS HUMAN GPCRS

1. Identification of Human GPCRs

15 Certain of the disclosed endogenous human GPCRs were identified based upon a review of the GenBank™ database information. While searching the database, the following cDNA clones were identified as evidenced below (Table C).

TABLE C

20	Disclosed Human Orphan GPCRs	Accession Number	Complete DNA Sequence (Base Pairs)	Open Reading Frame (Base Pairs)	Nucleic Acid SEQ.ID. NO.	Amino Acid SEQ.ID. NO.
	hARE-3	AL033379	111,389 bp	1,260 bp	1	2
	hARE-4	AC006087	226,925 bp	1,119 bp	3	4
25	hARE-5	AC006255	127,605 bp	1,104 bp	5	6
	hRUP3	AL035423	140,094 bp	1,005 bp	7	8

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hRUP5	AC005849	169,144 bp	1,413 bp	9	10
hRUP6	AC005871	218,807 bp	1,245 bp	11	12
hRUP7	AC007922	158,858 bp	1,173 bp	13	14

Other disclosed endogenous human GPCRs were identified by conducting a BLAST™ search of EST database (dbest) using the following EST clones as query sequences. The following EST clones identified were then used as a probe to screen a human genomic library (Table D).

TABLE D

	Disclosed Human Orphan GPCRs	Query (Sequence)	EST Clone/Accession No. Identified	Open Reading Frame (Base Pairs)	Nucleic Acid SEQ.ID.NO.	Amino Acid SEQ.ID.NO.
10	hGPCR27	Mouse GPCR27	AA775870	1,125 bp	17	18
	hARE-1	TDAG	1689643 AI090920	999 bp	19	20
15	hARE-2	GPCR27	68530 AA359504	1,122 bp	21	22
	hPPR1	Bovine PPR1	238667 H67224	1,053 bp	23	24
	hG2A	Mouse 1179426	See Example 2(a). below	1,113 bp	25	26
	hCHN3	N.A.	EST 36581 (full length)	1,113 bp	27	28
	hCHN4	TDAG	1184934 AA804531	1,077 bp	29	30
20	hCHN6	N.A.	EST 2134670 (full length)	1,503 bp	31	32
	hCHN8	KIAA0001	EST 764455	1,029 bp	33	34
	hCHN9	1365839	EST 1541536	1,077 bp	35	36
	hCHN10	Mouse EST 1365839	Human 1365839	1,005 bp	37	38
25	hRUP4	N.A.	AI307658	1,296 bp	39	40

N.A. = "not applicable".

2. Full Length Cloning

a. Human G2A

Mouse EST clone 1179426 was used to obtain a human genomic clone containing all

but three amino acid G2A coding sequences. The 5' of this coding sequence was obtained by using 5'RACE, and the template for PCR was Clontech's Human Spleen Marathon-Ready™ cDNA. The disclosed human G2A was amplified by PCR using the G2A cDNA specific primers for the first and second round PCR as shown in SEQ.ID.NO.: 41 and SEQ.ID.NO.:42
5 as follows:

5'-CTGTGTACAGCAGTCGCAGAGTG-3' (SEQ.ID.NO.: 41; 1st round PCR)

5'-GAGTGCCAGGCAGAGCAGGTAGAC-3' (SEQ.ID.NO.: 42; second round PCR).

PCR was performed using Advantage GC Polymerase Kit (Clontech; manufacturing instructions will be followed), at 94°C for 30 sec followed by 5 cycles of 94°C for 5 sec and
10 72°C for 4 min; and 30 cycles of 94° for 5 sec and 70° for 4 min. An approximate 1.3 Kb
PCR fragment was purified from agarose gel, digested with Hind III and Xba I and cloned into
the expression vector pRC/CMV2 (Invitrogen). The cloned-insert was sequenced using the
T7 Sequenase™ kit (USB Amersham; manufacturer instructions followed) and the sequence
was compared with the presented sequence. Expression of the human G2A was detected by
15 probing an RNA dot blot (Clontech; manufacturer instructions followed) with the P³²-labeled
fragment.

b. CHN9

Sequencing of the EST clone 1541536 showed CHN9 to be a partial cDNA clone having only an initiation codon; *i.e.*, the termination codon was missing. When CHN9
20 was used to blast against data base (nr), the 3' sequence of CHN9 was 100% homologous to the 5' untranslated region of the leukotriene B4 receptor cDNA, which contained a termination codon in the frame with CHN9 coding sequence. To determine whether the 5' untranslated region of LTB4R cDNA was the 3' sequence of CHN9, PCR was performed using primers based upon the 5' sequence flanking the initiation codon found in CHN9 and

the 3' sequence around the termination codon found in the LTB4R 5' untranslated region.

The 5' primer sequence utilized was as follows:

5'-CCCGAATT CCTGCTT GCTCCCAGCTTGGCCC-3' (SEQ.ID.NO.: 43; sense) and

5'-TGTGGATCCTGCTGTCAAAGGTCCCATTCCGG-3' (SEQ.ID.NO.: 44; antisense).

5 PCR was performed using thymus cDNA as a template and rTth polymerase (Perkin Elmer) with the buffer system provided by the manufacturer, 0.25 uM of each primer, and 0.2 mM of each 4 nucleotides. The cycle condition was 30 cycles of 94°C for 1 min, 65°C for 1 min and 72 °C for 1 min and 10 sec. A 1.1kb fragment consistent with the predicted size was obtained from PCR. This PCR fragment was subcloned into pCMV (see below) and
10 sequenced (see, SEQ.ID.NO.: 35).

c. RUP 4

The full length RUP4 was cloned by RT-PCR with human brain cDNA (Clontech) as templates:

5'-TCACAATGCTAGGTGTGGTC-3' (SEQ.ID.NO.: 45; sense) and

15 5'-TGCATAGACAATGGGATTACAG-3' (SEQ.ID.NO.: 46; antisense).

PCR was performed using TaqPlus Precision™ polymerase (Stratagene; manufacturing instructions followed) by the following cycles: 94 °C for 2 min; 94 °C 30 sec; 55 °C for 30 sec, 72 °C for 45 sec, and 72 °C for 10 min. Cycles 2 through 4 were repeated 30 times.

The PCR products were separated on a 1% agarose gel and a 500 bp PCR fragment
20 was isolated and cloned into the pCRII-TOPO™ vector (Invitrogen) and sequenced using the T7 DNA Sequenase™ kit (Amsham) and the SP6/T7 primers (Stratagene). Sequence analysis revealed that the PCR fragment was indeed an alternatively spliced form of AI307658 having a continuous open reading frame with similarity to other GPCRs. The completed sequence of this PCR fragment was as follows:

5'-TCACAATGCTAGGTGTGGCTGGCTGGCAGTCATCGTAGGATCACCCATGTGGCAC
GTGCAACAACCTGAGATCAAATATGACTTCTATATGAAAAGAACACATCTGCTGCTTAAGA
GTGGACCAGCCCTGTGCACCAGAACATCTACACCACCTTCATCCTTGTCATCCTCTCCTGC
CTCTTATGGTGATGCTTATTCTGTACGTAAAATTGGTTATGAACCTTGGATAAAGAAAAGAGTT
5 GGGGATGGTCAGTGCCTCGAACTATTGAAAAGAAATGTCCAAATAGCCAGGAAGAAG
AAACGAGCTGTCATTATGATGGTGACAGTGGTGGCTCTTTGCTGTGCTGGGCACCATTCC
ATGTTGTCCATATGATGATTGAATACAGTAATTTGAAAAGGAATATGATGATGTCACAATCAA
GATGATTTTGCTATGTGCAAATTATTGGATTITCCAACTCATCTGTAATCCCATTGTCTATGCA-
3' (SEQ.ID.NO.: 47)

10 Based on the above sequence, two sense oligonucleotide primer sets:

5'-CTGCTTAGAAGAGTGGACCAG-3' (SEQ.ID.NO.: 48; oligo 1),

5'-CTGTGCACCAGAACAGATCTACAC-3' (SEQ.ID.NO.: 49; oligo 2) and

two antisense oligonucleotide primer sets:

5'-CAAGGATGAAGGTGGTAGA-3' (SEQ.ID.NO.: 50; oligo 3)

15 5'-GTGTAGATCTTCTGGTGCACAGG-3' (SEQ.ID.NO.: 51; oligo 4)

were used for 3'- and 5'-RACE PCR with a human brain Marathon-Ready™ cDNA (Clontech, Cat# 7400-1) as template, according to manufacturer's instructions. DNA fragments generated by the RACE PCR were cloned into the pCRII-TOPO™ vector (Invitrogen) and sequenced using the SP6/T7 primers (Stratagene) and some internal primers.

20 The 3' RACE product contained a poly(A) tail and a completed open reading frame ending at a TAA stop codon. The 5' RACE product contained an incomplete 5' end; i.e., the ATG initiation codon was not present.

Based on the new 5' sequence, oligo 3 and the following primer:

5'-GCAATGCAGGTCAAGTGAGC-3' (SEQ.ID.NO.: 52; oligo 5)

25 were used for the second round of 5' race PCR and the PCR products were analyzed as above.

A third round of 5' race PCR was carried out utilizing antisense primers:

5'-TGGAGCATGGTGACGGGAATGCAGAAC-3' (SEQ.ID.NO.: 53; oligo 6) and

5'-GTGATGAGCAGGTCACTGAGCGCCAAG-3' (SEQ.ID.NO.: 54; oligo 7).

The sequence of the 5' RACE PCR products revealed the presence of the initiation codon

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ATG, and further round of 5' race PCR did not generate any more 5' sequence. The completed 5' sequence was confirmed by RT-PCR using sense primer

5'-GCAATGCAGGCGCTTAACATTAC-3' (SEQ.ID.NO.: 55; oligo 8)

and oligo 4 as primers and sequence analysis of the 650 bp PCR product generated from

5 human brain and heart cDNA templates (Clontech, Cat# 7404-1). The completed 3' sequence was confirmed by RT-PCR using oligo 2 and the following antisense primer:

5'-TTGGGTTACAATCTGAAGGGCA-3' (SEQ.ID.NO.:56; oligo 9)

and sequence analysis of the 670 bp PCR product generated from human brain and heart cDNA templates. (Clontech, Cat# 7404-1).

10

d. RUP5

The full length RUP5 was cloned by RT-PCR using a sense primer upstream from ATG, the initiation codon (SEQ.ID.NO.:57), and an antisense primer containing TCA as the stop codon (SEQ.ID.NO.:58), which had the following sequences:

5'-ACTCCGTGTCCAGCAGGACTCTG-3' (SEQ.ID.NO.: 57)

15

5'-TGCCTGTTCCCTGGACCCTCACGTG-3' (SEQ.ID.NO.: 58)

and human peripheral leukocyte cDNA (Clontech) as a template. Advantage™ cDNA polymerase (Clontech) was used for the amplification in a 50ul reaction by the following cycle with step 2 through step 4 repeated 30 times: 94°C for 30 sec; 94° for 15 sec; 69° for 40 sec; 72°C for 3 min; and 72°C fro 6 min. A 1.4kb PCR fragment was isolated and cloned with 20 the pCRII-TOPO™ vector (Invitrogen) and completely sequenced using the T7 DNA Sequenase™ kit (Amsham). *See*, SEQ.ID.NO.: 9.

e. RUP6

The full length RUP6 was cloned by RT-PCR using primers:

5'-CAGGCCTTGGATTTAACATGTCAGGGATGG-3' (SEQ.ID.NO.: 59) and

5'-GGAGAGTCAGCTCTGAAAGAATTCAAGG-3' (SEQ.ID.NO.: 60);
and human thymus Marathon-Ready™ cDNA (Clontech) as a template. Advantage cDNA polymerase (Clontech, according to manufacturer's instructions) was used for the amplification in a 50ul reaction by the following cycle: 94 °C for 30sec; 94 °C for 5 sec; 66 °C
5 for 40sec; 72 °C for 2.5 sec and 72 °C for 7 min. Cycles 2 through 4 were repeated 30 times.
A 1.3 Kb PCR fragment was isolated and cloned into the pCRII-TOPO™ vector (Invitrogen) and completely sequenced (*see*, SEQ.ID.NO.: 11) using the ABI Big Dye Terminator™ kit (P.E. Biosystem).

f. RUP7

10 The full length RUP7 was cloned by RT-PCR using primers:

5'-TGATGTGATGCCAGATACTAATAGCAC-3' (SEQ.ID.NO.: 61; sense) and
5'-CCTGATTCAATTAGGTGAGATTGAGAC-3' (SEQ.ID.NO.: 62; antisense)
and human peripheral leukocyte cDNA (Clontech) as a template. Advantage™ cDNA polymerase (Clontech) was used for the amplification in a 50 ul reaction by the following
15 cycle with step 2 to step 4 repeated 30 times: 94 °C for 2 minutes; 94 °C for 15 seconds; 60 °C for 20 seconds; 72 °C for 2 minutes; 72 °C for 10 minutes. A 1.25 Kb PCR fragment was isolated and cloned into the pCRII-TOPO™ vector (Invitrogen) and completely sequenced using the ABI Big Dye Terminator™ kit (P.E. Biosystem). *See*, SEQ.ID.NO.: 13.

3. Angiotensin II Type 1 Receptor ("AT1")

20 The endogenous human angiotensin II type 1 receptor ("AT1") was obtained by PCR using genomic DNA as template and rTth polymerase (Perkin Elmer) with the buffer system provided by the manufacturer, 0.25 µM of each primer, and 0.2 mM of each 4 nucleotides. The cycle condition was 30 cycles of 94°C for 1 min, 55°C for 1min and 72 °C for 1.5 min. The 5' PCR primer contains a HindIII site with the sequence:

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5'-CCCAAGCTTCCCCAGGTGTATTGAT-3' (SEQ.ID.NO.: 63)

and the 3` primer contains a BamHI site with the following sequence:

5'-GTTGGATCCACATAATGCATTTCTC-3' (SEQ.ID.NO.: 64).

The resulting 1.3 kb PCR fragment was digested with HindIII and BamHI and cloned into

- 5 HindIII-BamHI site of pCMV expression vector. The cDNA clone was fully sequenced. Nucleic acid (SEQ.ID.NO.: 65) and amino acid (SEQ.ID.NO.: 66) sequences for human AT1 were thereafter determined and verified.

4. GPR38

To obtain GPR38, PCR was performed by combining two PCR fragments, using
10 human genomic cDNA as template and rTth polymerase (Perkin Elmer) with the buffer system provided by the manufacturer, 0.25uM of each primer, and 0.2 mM of each 4 nucleotides. The cycle condition for each PCR reaction was 30 cycles of 94°C for 1 min, 62°C for 1min and 72°C for 2 min.

The first fragment was amplified with the 5` PCR primer that contained an end site
15 with the following sequence:

5'-ACCATGGGCAGCCCTGGAACGGCAGC-3' (SEQ.ID.NO.:67)

and a 3` primer having the following sequence:

5'-AGAACCAACCACCAAGCAGGACGCGGACGGTCTGCCGGTGG-3' (SEQ.ID.NO.:68).

- The second PCR fragment was amplified with a 5` primer having the following sequence:
20 5'-GTCCCGCGTCCTGCTGGTGGTCTGGCATTATAATT-3' (SEQ.ID.NO.: 69)

and a 3` primer that contained a BamHI site and having the following sequence:

5'-CCTGGATCCTTATCCCATCGTCTCACGTTAGC-3' (SEQ.ID.NO.: 70).

The two fragments were used as templates to amplify GPR38, using SEQ.ID.NO.: 67 and SEQ.ID.NO.: 70 as primers (using the above-noted cycle conditions). The resulting 1.44kb

PCR fragment was digested with BamHI and cloned into Blunt-BamHI site of pCMV expression vector.

5. MC4

To obtain MC4, PCR was performed using human genomic cDNA as template and 5 rTth polymerase (Perkin Elmer) with the buffer system provided by the manufacturer, 0.25uM of each primer, and 0.2 mM of each 4 nucleotides. The cycle condition for each PCR reaction was 30 cycles of 94°C for 1 min, 54°C for 1min and 72°C for 1.5 min.

The 5' PCR contained an EcoRI site with the sequence:

5'-CTGGAATTCTCCTGCCAGCATGGTGA-3' (SEQ.ID.NO.: 71)

10 and the 3' primer contained a BamHI site with the sequence:

5'-GCAGGATCCTATATTGCGTGCTCTGTCCCC-3' (SEQ.ID.NO.: 72).

The 1.0 kb PCR fragment was digest with EcoRI and BamHI and cloned into EcoRI-BamHI site of pCMV expression vector. Nucleic acid (SEQ.ID.NO.: 73) and amino acid (SEQ.ID.NO.: 74) sequences for human MC4 were thereafter determined.

15 6. CCKB

To obtain CCKB, PCR was performed using human stomach cDNA as template and rTth polymerase (Perkin Elmer) with the buffer system provided by the manufacturer, 0.25uM of each primer, and 0.2 mM of each 4 nucleotides. The cycle condition for each PCR reaction was 30 cycles of 94°C for 1 min, 65°C for 1min and 72°C for 1 min and 30 sec.

20 The 5' PCR contained a HindIII site with the sequence:

5'-CCGAAGCTTCGAGCTGAGTAAGGCGGCGGGCT-3' (SEQ.ID.NO.: 75)

and the 3' primer contained an EcoRI site with the sequence:

5'-GTGGAATTCAATTGCCCTGCCTCAACCCCCA-3 (SEQ.ID.NO.: 76).

The resulting 1.44 kb PCR fragment was digest with HindIII and EcoRI and cloned into

HindIII-EcoRI site of pCMV expression vector. Nucleic acid (SEQ.ID.NO.: 77) and amino acid (SEQ.ID.NO.: 78) sequences for human CCKB were thereafter determined.

7. TDAG8

To obtain TDAG8, PCR was performed using genomic DNA as template and rTth polymerase (Perkin Elmer) with the buffer system provided by the manufacturer, 0.25 µM of each primer, and 0.2 mM of each 4 nucleotides. The cycle condition was 30 cycles of 94°C for 1 min, 56°C for 1 min and 72 °C for 1 min and 20 sec. The 5' PCR primer contained a HindIII site with the following sequence:

5'-TGCAAGCTTAAAAGGAAAAATGAACAGC-3' (SEQ.ID.NO.: 79)

and the 3' primer contained a BamHI site with the following sequence:

5'-TAAGGATCCCTCCCTCAAAACATCCTTG -3' (SEQ.ID.NO.: 80).

The resulting 1.1 kb PCR fragment was digested with HindIII and BamHI and cloned into HindIII-BamHI site of pCMV expression vector. Three resulting clones sequenced contained three potential polymorphisms involving changes of amino acid 43 from Pro to Ala, amino acid 97 from Lys to Asn and amino acid 130 from Ile to Phe. Nucleic acid (SEQ.ID.NO.: 81) and amino acid (SEQ.ID.NO.: 82) sequences for human TDAG8 were thereafter determined.

8. H9

To obtain H9, PCR was performed using pituitary cDNA as template and rTth polymerase (Perkin Elmer) with the buffer system provided by the manufacturer, 0.25 µM of each primer, and 0.2 mM of each 4 nucleotides. The cycle condition was 30 cycles of 94°C for 1 min, 62°C for 1 min and 72°C for 2 min. The 5' PCR primer contained a HindIII site with the following sequence:

5'-GGAAAGCTAACGATCCCCAGGAGCACAT-3' (SEQ.ID.NO.: 15)

and the 3' primer contained a BamHI site with the following sequence:

5'-CTGGGATCCTACGAGAGCATTTTCACACAG-3' (SEQ.ID.NO.:16).

The resulting 1.9 kb PCR fragment was digested with HindIII and BamHI and cloned into HindIII-BamHI site of pCMV expression vector. H9 contained three potential polymorphisms involving changes of amino acid P320S, S493N and amino acid G448A. Nucleic acid 5 (SEQ.ID.NO.: 139) and amino acid (SEQ.ID.NO.: 140) sequences for human H9 were thereafter determined and verified.

Example 2

PREPARATION OF NON-ENDOGENOUS, CONSTITUTIVELY ACTIVATED GPCRS

Those skilled in the art are credited with the ability to select techniques for 10 mutation of a nucleic acid sequence. Presented below are approaches utilized to create non-endogenous versions of several of the human GPCRs disclosed above. The mutations disclosed below are based upon an algorithmic approach whereby the 16th amino acid (located in the IC3 region of the GPCR) from a conserved proline residue (located in the TM6 region of the GPCR, near the TM6/IC3 interface) is mutated, most preferably to a 15 lysine amino acid residue.

1. Transformer Site-Directed™ Mutagenesis

Preparation of non-endogenous human GPCRs may be accomplished on human 20 GPCRs using Transformer Site-Directed™ Mutagenesis Kit (Clontech) according to the manufacturer instructions. Two mutagenesis primers are utilized, most preferably a lysine mutagenesis oligonucleotide that creates the lysine mutation, and a selection marker oligonucleotide. For convenience, the codon mutation to be incorporated into the human GPCR is also noted, in standard form (Table E):

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TABLE E

	Receptor Identifier	Codon Mutation
5	hARE-3	F313K
	hARE-4	V233K
	hARE-5	A240K
	hGPCR14	L257K
	hGPCR27	C283K
10	hARE-1	E232K
	hARE-2	G285K
	hPPR1	L239K
	hG2A	K232A
	hRUP3	L224K
	hRUP5	A236K
	hRUP6	N267K
15	hRUP7	A302K
	hCHN4	V236K
	hMC4	A244K
	hCHN3	S284K
	hCHN6	L352K
20	hCHN8	N235K
	hCHN9	G223K
	hCHN10	L231K
	hH9	F236K

The following GPCRs were mutated according with the above method using the
25 designated sequence primers (Table F).

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TABLE F

Receptor Identifier	Codon Mutation	Lysine Mutagenesis (SEQ.ID.NO.) 5'-3' orientation, mutation sequence underlined	Selection Marker (SEQ.ID.NO.) 5'-3' orientation
5	hRUP4	V272K	CAGGAAGAAG <u>AAAC</u> GAGC TGTCA <u>TATG</u> A <u>TGGT</u> GACA GTG (83)
	hAT1	<i>see below</i>	alternative approach; <i>see below</i>
	hGPR38	V297K	GGCCACCGGCAGAC <u>CCAAAC</u> GCGTC <u>CTG</u> C <u>TG</u> (85)
	hCCKB	V332K	alternative approach; <i>see below</i>
	hTDAG8	I225K	GGAAAAGAAGAGAAC <u>AA</u> <u>AA</u> AA <u>ACTACT</u> GT <u>CAGC</u> ATC (87)
	hH9	F236K	GCTGAGGTT <u>CGCA</u> <u>ATAA</u> <u>AC</u> TAACC <u>ATG</u> TT <u>GTG</u> (143)
	hMC4	A244K	GCCAATAT <u>GAAGGG</u> <u>AAA</u> ATTAC <u>CTTGACC</u> ATC (137)

10

The non-endogenous human GPCRs were then sequenced and the derived and verified nucleic acid and amino acid sequences are listed in the accompanying "Sequence Listing" appendix to this patent document, as summarized in Table G below:

TABLE G

	Non Endogenous Human GPCR	Nucleic Acid Sequence Listing	Amino Acid Sequence Listing
15	hRUP4 (V272K)	SEQ.ID.NO.: 127	SEQ.ID.NO.: 128
20	hAT1 <i>(see alternative approaches below)</i>	<i>(see alternative approaches below)</i>	<i>(see alternative approaches below)</i>
25	hGPR38 (V297K)	SEQ.ID.NO.: 129	SEQ.ID.NO.: 130
	hCCKB (V332K)	SEQ.ID.NO.: 131	SEQ.ID.NO.: 132
	HTDAG8 (I225K)	SEQ.ID.NO.: 133	SEQ.ID.NO.: 134
30	hH9 (F236K)	SEQ.ID.NO.: 141	SEQ.ID.NO.: 142
	hMC4 (A244K)	SEQ.ID.NO.: 135	SEQ.ID.NO.: 136

2. Alternative Approaches For Creation of Non-Endogenous Human GPCRs

a. AT1

1. F239K Mutation

Preparation of a non-endogenous, constitutively activated human AT1 receptor was accomplished by creating an F239K mutation (see, SEQ.ID.NO.: 89 for nucleic acid sequence, and SEQ.ID.NO.: 90 for amino acid sequence). Mutagenesis was performed using Transformer Site-Directed Mutagenesis™ Kit (Clontech) according to the manufacturer's instructions. The two mutagenesis primers were used, a lysine mutagenesis oligonucleotide (SEQ.ID.NO.: 91) and a selection marker oligonucleotide (SEQ.ID.NO.: 92), which had the following sequences:

5'-CCAAGAAATGATGATATTAAAAAGATAATTATGGC-3' (SEQ.ID.NO.: 91)

5'-CTCCTCGGTCCCTATCGTTGTCAGAAGT-3' (SEQ.ID.NO.: 92),

respectively.

2. N111A Mutation

Preparation of a non-endogenous human AT1 receptor was also accomplished by creating an N111A mutation (see, SEQ.ID.NO.: 93 for nucleic acid sequence, and SEQ.ID.NO.: 94 for amino acid sequence). Two PCR reactions were performed using pfu polymerase (Stratagene) with the buffer system provided by the manufacturer, supplemented with 10% DMSO, 0.25 µM of each primer, and 0.5 mM of each 4 nucleotides. The 5' PCR sense primer used had the following sequence:

5'-CCCAAGCTTCCCCAGGTGTATTTGAT-3' (SEQ.ID.NO.: 95)

and the antisense primer had the following sequence:

5'-CCTGCAGCGAAACTGACTCTGGCTGAAG-3' (SEQ.ID.NO.: 96).

The resulting 400 bp PCR fragment was digested with HindIII site and subcloned into HindIII-SmaI site of pCMV vector (5' construct). The 3' PCR sense primer used had the following sequence:

5 5'-CTGTACGCTAGTGTGTTCTACTCACGTGTCAGCATTGAT-3' (SEQ.ID.NO.: 97)

and the antisense primer had the following sequence:

5'-GTTGGATCCACATAATGCATTTCTC-3' (SEQ.ID.NO.: 98)

The resulting 880 bp PCR fragment was digested with BamHI and inserted into Pst (blunted by T4 polymerase) and BamHI site of 5' construct to generated the full length
10 1111A construct. The cycle condition was 25 cycles of 94°C for 1 min, 60°C for 1min and 72 °C for 1 min (5' PCR) or 1.5 min (3' PCR).

3. AT2K255IC3 Mutation

Preparation of a non-endogenous, constitutively activated human AT1 was accomplished by creating an AT2K255IC3 "domain swap" mutation (see, SEQ.ID.NO.:99
15 for nucleic acid sequence, and SEQ.ID.NO.: 100 for amino acid sequence). Restriction sites flanking IC3 of AT1 were generated to facilitate replacement of the IC3 with corresponding IC3 from angiotensin II type 2 receptor (AT2). This was accomplished by performing two PCR reactions. A 5' PCR fragment (Fragment A) encoded from the 5'
20 untranslated region to the beginning of IC3 was generated by utilizing SEQ.ID.NO.: 63 as sense primer and the following sequence:

5'-TCCGAATTCCAAAATAACTTGTAAGAATGATCAGAAA-3' (SEQ.ID.NO.: 101)

as antisense primer. A 3' PCR fragment (Fragment B) encoding from the end of IC3 to the 3' untranslated region was generated by using the following sequence:

5'-AGATCTTAAGAAGATAATTATGGCAATTGTGCT-3' (SEQ.ID.NO.: 102)

as sense primer and SEQ.ID.NO.: 64 as antisense primer. The PCR condition was 30 cycles of 94°C for 1 min, 55°C for 1min and 72 °C for 1.5 min using endogenous AT1 cDNA clone as template and pfu polymerase (Stratagene), with the buffer systems provided by the manufacturer, supplemented with 10% DMSO, 0.25 µM of each primer, 5 and 0.5 mM of each 4 nucleotides. Fragment A (720 bp) was digested with HindIII and EcoRI and subcloned. Fragment B was digested with BamHI and subcloned into pCMV vector with an EcoRI site 5' to the cloned PCR fragment.

The DNA fragment (Fragment C) encoding IC3 of AT2 with a L255K mutation and containing an EcoRI cohesive end at 5' and a AflII cohesive end at 3', was generated 10 by annealing 2 synthetic oligonucleotides having the following sequences:

5'AATTCGAAAACACTTACTGAAGACGAATAGCTATGGGAAGAACAGGATAACCCGTGACCAA
G-3' (sense; SEQ.ID.NO.: 103)
5'TTAACTTGGTCACGGTTATCCTGTTCCCAGCTATTGCTTCAGT
15 AAGTGTTTCG-3' (antisense; SEQ.ID.NO.: 104).

Fragment C was inserted in front of Fragment B through EcoRI and AflII site. The resulting clone was then ligated with the Fragment A through the EcoRI site to generate AT1 with AT2K255IC3.

4. A243+ Mutation

20 Preparation of a non-endogenous human AT1 receptor was also accomplished by creating an A243+ mutation (see, SEQ.ID.NO.: 105 for nucleic acid sequence, and SEQ.ID.NO.: 106 for amino acid sequence). An A243+ mutation was constructed using the following PCR based strategy: Two PCR reactions was performed using pfu polymerase (Stratagene) with the buffer system provided by the manufacturer supplemented with 10% 25 DMSO, 0.25 µM of each primer, and 0.5 mM of each 4 nucleotides. The 5' PCR sense primer

utilized had the following sequence:

5'-CCCAAGCTTCCCCAGGTGTATTTGAT-3' (SEQ.ID.NO.: 107)

and the antisense primer had the following sequence:

5'-AAGCACAATTGCTGCATAATTATCTTAAAAATATCATC-3' (SEQ.ID.NO.: 108).

5 The 3' PCR sense primer utilized had the following sequence:

5'-AAGATAATTATGGCAGCAATTGTGCTTTCTTTCTT-3' (SEQ.ID.NO.: 109)

containing the Ala insertion and antisense primer:

5'-GTTGGATCCACATAATGCATTTC-3'(SEQ.ID.NO.: 110).

The cycle condition was 25 cycles of 94°C for 1 min, 54°C for 1min and 72 °C for 1.5 min.

10 An aliquot of the 5' and 3' PCR were then used as co-template to perform secondary PCR using the 5' PCR sense primer and 3' PCR antisense primer. The PCR condition was the same as primary PCR except the extention time was 2.5 min. The resulting PCR fragment was digested with HindIII and BamHI and subcloned into pCMV vector. (See, SEQ.ID.NO.: 105)

15 **4. CCKB**

Preparation of the non-endogenous, constitutively activated human CCKB receptor was accomplished by creating a V322K mutation (see, SEQ.ID.NO.: 111 for nucleic acid sequence and SEQ.ID.NO.: 112 for amino acid sequence). Mutagenesis was performed by PCR via amplification using the wildtype CCKB from Example 1.

20 The first PCR fragment (1kb) was amplified by using SEQ.ID.NO.: 75 and an antisense primer comprising a V322K mutation:

5'-CAGCAGCATGCGCTTCACGCGCTTCTAGCCCAG-3' (SEQ.ID.NO.: 113).

The second PCR fragment (0.44kb) was amplified by using a sense primer comprising the V322K mutation:

5'-AGAACGCGTGAAGCGCATGCTGCTGGTATCGTT-3' (SEQ.ID.NO.: 114) and SEQ.ID.NO.: 76.

The two resulting PCR fragments were then used as template for amplifying CCKB comprising V332K, using SEQ.ID.NO.: 75 and SEQ.ID.NO.: 76 and the above-noted 5 system and conditions. The resulting 1.44kb PCR fragment containing the V332K mutation was digested with HindIII and EcoRI and cloned into HindIII-EcoRI site of pCMV expression vector. (See, SEQ.ID.NO.: 111).

3. QuikChange™ Site-Directed™ Mutagenesis

Preparation of non-endogenous human GPCRs can also be accomplished by using 10 QuikChange™ Site-Directed™ Mutagenesis Kit (Stratagene, according to manufacturer's instructions). Endogenous GPCR is preferably used as a template and two mutagenesis primers utilized, as well as, most preferably, a lysine mutagenesis oligonucleotide and a selection marker oligonucleotide (included in kit). For convenience, the codon mutation incorporated into the human GPCR and the respective oligonucleotides are noted, in standard 15 form (Table H):

TABLE H

Receptor Identifier	Codon Mutation	Lysine Mutagenesis (SEQ.ID.NO.) 5'-3' orientation, mutation underlined	Selection Marker (SEQ.ID.NO.) 5'-3' orientation
hCHN3	S284K	ATGGAGAAAAGAAT <u>CAA</u> AAGAA TGTTCATATA (115)	TATATAGAACATTTTT GATTCTTTCTCCAT (116)
hCHN6	L352K	CGCTCTCTGGCCTTG <u>AAG</u> CGCAC GCTCAGC (117)	GCTGAGCGTGCCTCA AGGCCAGAGAGCG (118)
5 hCHN8	N235K	CCCAGGAAAAGGTG <u>AAAG</u> TCA AAGTTTTC (119)	AAAAACTTGACTTCAC CTTTTCCCTGGG (120)
hCHN9	G223K	GGGGCGCGGGTG <u>AAAC</u> GGCTGG TGAGC (121)	GCTCACCAGCCGTTCA CCCGCGCCCC (122)
hCHN10	L231K	CCCCTTG <u>AAAG</u> CCTAAGAACTT GGTCATC (123)	GATGACCAAGTTCTTAG GCTTTCAAGGGG (124)

Example 3
RECEPTOR EXPRESSION

10 Although a variety of cells are available to the art for the expression of proteins, it is most preferred that mammalian cells be utilized. The primary reason for this is predicated upon practicalities, *i.e.*, utilization of, *e.g.*, yeast cells for the expression of a GPCR, while possible, introduces into the protocol a non-mammalian cell which may not (indeed, in the case of yeast, does not) include the receptor-coupling, genetic-mechanism and secretary pathways that have evolved for mammalian systems – thus, results obtained in non-mammalian cells, while of potential use, are not as preferred as that obtained from mammalian cells. Of the mammalian cells, COS-7, 293 and 293T cells are particularly preferred, although the specific mammalian cell utilized can be predicated upon the particular needs of the artisan.

15

On day one, 1×10^7 293T cells per 150mm plate were plated out. On day two, two reaction tubes were prepared (the proportions to follow for each tube are per plate): tube A was prepared by mixing 20 μ g DNA (*e.g.*, pCMV vector; pCMV vector with receptor cDNA, etc.) in 1.2ml serum free DMEM (Irvine Scientific, Irvine, CA); tube B was

prepared by mixing 120 μ l lipofectamine (Gibco BRL) in 1.2ml serum free DMEM. Tubes A and B were admixed by inversions (several times), followed by incubation at room temperature for 30-45min. The admixture is referred to as the "transfection mixture". Plated 293T cells were washed with 1XPBS, followed by addition of 10ml serum free 5 DMEM. 2.4ml of the transfection mixture were added to the cells, followed by incubation for 4hrs at 37°C/5% CO₂. The transfection mixture was removed by aspiration, followed by the addition of 25ml of DMEM/10% Fetal Bovine Serum. Cells were incubated at 37°C/5% CO₂. After 72hr incubation, cells were harvested and utilized for analysis.

Example 4**10 ASSAYS FOR DETERMINATION OF CONSTITUTIVE ACTIVITY
OF NON-ENDOGENOUS GPCRs**

A variety of approaches are available for assessment of constitutive activity of the non-endogenous human GPCRs. The following are illustrative; those of ordinary skill in the art are credited with the ability to determine those techniques that are preferentially 15 beneficial for the needs of the artisan.

1. Membrane Binding Assays: [³⁵S]GTP γ S Assay

When a G protein-coupled receptor is in its active state, either as a result of ligand binding or constitutive activation, the receptor couples to a G protein and stimulates the release of GDP and subsequent binding of GTP to the G protein. The alpha subunit of the G 20 protein-receptor complex acts as a GTPase and slowly hydrolyzes the GTP to GDP, at which point the receptor normally is deactivated. Constitutively activated receptors continue to exchange GDP for GTP. The non-hydrolyzable GTP analog, [³⁵S]GTP γ S, can be utilized to demonstrate enhanced binding of [³⁵S]GTP γ S to membranes expressing constitutively activated receptors. The advantage of using [³⁵S]GTP γ S binding to measure constitutive

activation is that: (a) it is generically applicable to all G protein-coupled receptors; (b) it is proximal at the membrane surface making it less likely to pick-up molecules which affect the intracellular cascade.

The assay utilizes the ability of G protein coupled receptors to stimulate [³⁵S]GTP γ S binding to membranes expressing the relevant receptors. The assay can, therefore, be used in the direct identification method to screen candidate compounds to known, orphan and constitutively activated G protein-coupled receptors. The assay is generic and has application to drug discovery at all G protein-coupled receptors.

The [³⁵S]GTP γ S assay can be incubated in 20 mM HEPES and between 1 and about 10 20mM MgCl₂ (this amount can be adjusted for optimization of results, although 20mM is preferred) pH 7.4, binding buffer with between about 0.3 and about 1.2 nM [³⁵S]GTP γ S (this amount can be adjusted for optimization of results, although 1.2 is preferred) and 12.5 to 75 μ g membrane protein (*e.g.* COS-7 cells expressing the receptor; this amount can be adjusted for optimization, although 75 μ g is preferred) and 1 μ M GDP (this amount can be changed for 15 optimization) for 1 hour. Wheatgerm agglutinin beads (25 μ l; Amersham) should then be added and the mixture incubated for another 30 minutes at room temperature. The tubes are then centrifuged at 1500 x g for 5 minutes at room temperature and then counted in a scintillation counter.

A less costly but equally applicable alternative has been identified which also meets 20 the needs of large scale screening. Flash platesTM and WallacTM scintistrips may be utilized to format a high throughput [³⁵S]GTP γ S binding assay. Furthermore, using this technique, the assay can be utilized for known GPCRs to simultaneously monitor tritiated ligand binding to the receptor at the same time as monitoring the efficacy via [³⁵S]GTP γ S binding. This is

possible because the Wallac beta counter can switch energy windows to look at both tritium and ^{35}S -labeled probes. This assay may also be used to detect other types of membrane activation events resulting in receptor activation. For example, the assay may be used to monitor ^{32}P phosphorylation of a variety of receptors (both G protein coupled and tyrosine kinase receptors). When the membranes are centrifuged to the bottom of the well, the bound $[^{35}\text{S}]G\text{TP}\gamma\text{S}$ or the ^{32}P -phosphorylated receptor will activate the scintillant which is coated of the wells. Scinti® strips (Wallac) have been used to demonstrate this principle. In addition, the assay also has utility for measuring ligand binding to receptors using radioactively labeled ligands. In a similar manner, when the radiolabeled bound ligand is centrifuged to the bottom of the well, the scintistrip label comes into proximity with the radiolabeled ligand resulting in activation and detection.

2. Adenylyl Cyclase

A Flash Plate™ Adenylyl Cyclase kit (New England Nuclear; Cat. No. SMP004A) designed for cell-based assays can be modified for use with crude plasma membranes. The Flash Plate wells contain a scintillant coating which also contains a specific antibody recognizing cAMP. The cAMP generated in the wells was quantitated by a direct competition for binding of radioactive cAMP tracer to the cAMP antibody. The following serves as a brief protocol for the measurement of changes in cAMP levels in membranes that express the receptors.

Transfected cells are harvested approximately three days after transfection. Membranes were prepared by homogenization of suspended cells in buffer containing 20mM HEPES, pH 7.4 and 10mM MgCl₂. Homogenization is performed on ice using a Brinkman Polytron™ for approximately 10 seconds. The resulting homogenate is centrifuged at 49,000

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X g for 15 minutes at 4°C. The resulting pellet is then resuspended in buffer containing 20mM HEPES, pH 7.4 and 0.1 mM EDTA, homogenized for 10 seconds, followed by centrifugation at 49,000 X g for 15 minutes at 4°C. The resulting pellet can be stored at -80°C until utilized. On the day of measurement, the membrane pellet is slowly thawed at room temperature, resuspended in buffer containing 20mM HEPES, pH 7.4 and 10mM MgCl₂ (these amounts can be optimized, although the values listed herein are preferred), to yield a final protein concentration of 0.60mg/ml (the resuspended membranes were placed on ice until use).

cAMP standards and Detection Buffer (comprising 2 µCi of tracer [¹²⁵I] cAMP (100 µl) to 11 ml Detection Buffer) are prepared and maintained in accordance with the manufacturer's instructions. Assay Buffer is prepared fresh for screening and contained 20mM HEPES, pH 7.4, 10mM MgCl₂, 20mM (Sigma), 0.1 units/ml creatine phosphokinase (Sigma), 50 µM GTP (Sigma), and 0.2 mM ATP (Sigma); Assay Buffer can be stored on ice until utilized. The assay is initiated by addition of 50ul of assay buffer followed by addition of 50ul of membrane suspension to the NEN Flash Plate. The resultant assay mixture is incubated for 60 minutes at room temperature followed by addition of 100ul of detection buffer. Plates are then incubated an additional 2-4 hours followed by counting in a Wallac MicroBeta™ scintillation counter. Values of cAMP/well are extrapolated from a standard cAMP curve that is contained within each assay plate.

20

C. Reporter-Based Assays

1. CREB Reporter Assay (Gs-associated receptors)

A method to detect Gs stimulation depends on the known property of the transcription factor CREB, which is activated in a cAMP-dependent manner. A PathDetect™ CREB trans-

Reporting System (Stratagene, Catalogue # 219010) can utilized to assay for Gs coupled activity in 293 or 293T cells. Cells are transfected with the plasmids components of this above system and the indicated expression plasmid encoding endogenous or mutant receptor using a Mammalian Transfection Kit (Stratagene, Catalogue #200285) according to the manufacturer's instructions. Briefly, 400 ng pFR-Luc (luciferase reporter plasmid containing Gal4 recognition sequences), 40 ng pFA2-CREB (Gal4-CREB fusion protein containing the Gal4 DNA-binding domain), 80 ng pCMV-receptor expression plasmid (comprising the receptor) and 20 ng CMV-SEAP (secreted alkaline phosphatase expression plasmid: alkaline phosphatase activity is measured in the media of transfected cells to control for variations in transfection efficiency between samples) are combined in a calcium phosphate precipitate as per the Kit's instructions. Half of the precipitate is equally distributed over 3 wells in a 96-well plate, kept on the cells overnight, and replaced with fresh medium the following morning. Forty-eight (48) hr after the start of the transfection, cells are treated and assayed for, e.g., luciferase activity

15

2. AP1 reporter assay (Gq-associated receptors)

A method to detect Gq stimulation depends on the known property of Gq-dependent phospholipase C to cause the activation of genes containing AP1 elements in their promoter. A Pathdetect™ AP-1 cis-Reporting System (Stratagene, Catalogue # 219073) can be utilized following the protocol set forth above with respect to the CREB reporter assay, except that the components of the calcium phosphate precipitate were 410 ng pAP1-Luc, 80 ng pCMV-receptor expression plasmid, and 20 ng CMV-SEAP.

3. CRE-LUC Reporter Assay

293 and 293T cells are plated-out on 96 well plates at a density of 2×10^4 cells per

well and were transfected using Lipofectamine Reagent (BRL) the following day according to manufacturer instructions. A DNA/lipid mixture is prepared for each 6-well transfection as follows: 260ng of plasmid DNA in 100 μ l of DMEM were gently mixed with 2 μ l of lipid in 100 μ l of DMEM (the 260ng of plasmid DNA consisted of 200ng of a 8xCRE-Luc reporter 5 plasmid (*see* below and Figure 1 for a representation of a portion of the plasmid), 50ng of pCMV comprising endogenous receptor or non-endogenous receptor or pCMV alone, and 10ng of a GPRS expression plasmid (GPRS in pcDNA3 (Invitrogen)). The 8XCRE-Luc reporter plasmid was prepared as follows: vector SRIF- β -gal was obtained by cloning the rat somatostatin promoter (-71/+51) at BglIV-HindIII site in the p β gal-Basic Vector (Clontech). 10 Eight (8) copies of cAMP response element were obtained by PCR from an adenovirus template AdpCF126CCRE8 (*see*, 7 Human Gene Therapy 1883 (1996)) and cloned into the SRIF- β -gal vector at the Kpn-BglIV site, resulting in the 8xCRE- β -gal reporter vector. The 8xCRE-Luc reporter plasmid was generated by replacing the beta-galactosidase gene in the 8xCRE- β -gal reporter vector with the luciferase gene obtained from the pGL3-basic vector 15 (Promega) at the HindIII-BamHI site. Following 30 min. incubation at room temperature, the DNA/lipid mixture was diluted with 400 μ l of DMEM and 100 μ l of the diluted mixture was added to each well. 100 μ l of DMEM with 10% FCS were added to each well after a 4hr incubation in a cell culture incubator. The following day the transfected cells were changed with 200 μ l/well of DMEM with 10% FCS. Eight (8) hours later, the wells were changed to 20 100 μ l /well of DMEM without phenol red, after one wash with PBS. Luciferase activity were measured the next day using the LucLite™ reporter gene assay kit (Packard) following manufacturer instructions and read on a 1450 MicroBeta™ scintillation and luminescence counter (Wallac).

4. SRF-LUC Reporter Assay

One method to detect Gq stimulation depends on the known property of Gq-dependent phospholipase C to cause the activation of genes containing serum response factors in their promoter. A Pathdetect™ SRF-Luc-Reporting System (Stratagene) can be utilized to assay 5 for Gq coupled activity in, e.g., COS7 cells. Cells are transfected with the plasmid components of the system and the indicated expression plasmid encoding endogenous or non-endogenous GPCR using a Mammalian Transfection™ Kit (Stratagene, Catalogue #200285) according to the manufacturer's instructions. Briefly, 410 ng SRF-Luc, 80 ng pCMV-receptor expression plasmid and 20 ng CMV-SEAP (secreted alkaline phosphatase expression plasmid: 10 alkaline phosphatase activity is measured in the media of transfected cells to control for variations in transfection efficiency between samples) are combined in a calcium phosphate precipitate as per the manufacturer's instructions. Half of the precipitate is equally distributed over 3 wells in a 96-well plate, kept on the cells in a serum free media for 24 hours. The last 5 hours the cells are incubated with 1 μ M Angiotensin, where indicated. Cells are then lysed 15 and assayed for luciferase activity using a Luclite™ Kit (Packard, Cat. # 6016911) and "Trilux 1450 Microbeta" liquid scintillation and luminescence counter (Wallac) as per the manufacturer's instructions. The data can be analyzed using GraphPad Prism™ 2.0a (GraphPad Software Inc.).

5. Intracellular IP₃ Accumulation Assay

20 On day 1, cells comprising the receptors (endogenous and/or non-endogenous) can be plated onto 24 well plates, usually 1x10⁵ cells/well (although his umber can be optimized. On day 2 cells can be transfected by firstly mixing 0.25ug DNA in 50 ul serum free DMEM/well and 2 ul lipofectamine in 50 μ l serumfree DMEM/well. The solutions

are gently mixed and incubated for 15-30 min at room temperature. Cells are washed with 0.5 ml PBS and 400 μ l of serum free media is mixed with the transfection media and added to the cells. The cells are then incubated for 3-4 hrs at 37°C/5%CO₂ and then the transfection media is removed and replaced with 1ml/well of regular growth media. On 5 day 3 the cells are labeled with ³H-myo-inositol. Briefly, the media is removed and the cells are washed with 0.5 ml PBS. Then 0.5 ml inositol-free/serum free media (GIBCO BRL) is added/well with 0.25 μ Ci of ³H-myo-inositol / well and the cells are incubated for 16-18 hrs o/n at 37°C/5%CO₂. On Day 4 the cells are washed with 0.5 ml PBS and 0.45 ml of assay medium is added containing inositol-free/serum free media 10 μ M pargyline 10 10 mM lithium chloride or 0.4 ml of assay medium and 50 μ l of 10x ketanserin (ket) to final concentration of 10 μ M. The cells are then incubated for 30 min at 37°C. The cells are then washed with 0.5 ml PBS and 200 μ l of fresh/icecold stop solution (1M KOH; 18 mM Na-borate; 3.8 mM EDTA) is added/well. The solution is kept on ice for 5-10 min or until cells were lysed and then neutralized by 200 μ l of fresh/ice cold neutralization sol. 15 (7.5 % HCL). The lysate is then transferred into 1.5 ml eppendorf tubes and 1 ml of chloroform/methanol (1:2) is added/tube. The solution is vortexed for 15 sec and the upper phase is applied to a Biorad AG1-X8™ anion exchange resin (100-200 mesh). Firstly, the resin is washed with water at 1:1.25 W/V and 0.9 ml of upper phase is loaded onto the column. The column is washed with 10 mls of 5 mM myo-inositol and 10 ml of 5 20 mM Na-borate/60mM Na-formate. The inositol tris phosphates are eluted into scintillation vials containing 10 ml of scintillation cocktail with 2 ml of 0.1 M formic acid/ 1 M ammonium formate. The columns are regenerated by washing with 10 ml of 0.1 M formic acid/3M ammonium formate and rinsed twice with dd H₂O and stored at 4°C in water.

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Exemplary results are presented below in Table I:

TABLE I

Receptor	Mutation	Assay Utilized	Signal Generated: Endogenous Version (Relative Light Units)	Signal Generated: Non-Endogenous Version (Relative Light Units)	Percent Difference
hAT1	F239K	SRF-LUC	34	137	75%†
	AT2K255IC3	SRF-LUC	34	127	73%†
5 hTDAG8	I225K	CRE-LUC (293 cells)	2,715	14,440	81%†
	I225K	CRE-LUC (293T cells)	65,681	185,636	65%†
hH9 hCCKB	F236K V332K	CRE-LUC CRE-LUC	1,887 785	6,096 3,223	69%† 76%†

C. CELL-BASED DETECTION ASSAY (EXAMPLE -TDAG8)

10 293 cells were plated-out on 150mm plates at a density of 1.3×10^7 cells per plate, and were transfected using 12ug of the respective DNA and 60ul of Lipofectamine Reagent (BRL) per plate. The transfected cells were grown in media containing serum for an assay performed 24 hours post-transfection. For detection assay performed 48 hours post-transfection (assay comparing serum and serum-free media; see Figure 3), the initial media 15 was changed to either serum or serum-free media. The serum-free media was comprised solely of Dulbecco's Modified Eagle's (DME) High Glucose Medium (Irvine Scientific #9024). In addition to the above DME Medium, the media with serum contained the following: 10% Fetal Bovine Serum (Hyclone #SH30071.03), 1% of 100mM Sodium Pyruvate (Irvine Scientific #9334), 1% of 20mM L-Glutamine (Irvine Scientific #9317), and 1% of Penicillin-

Streptomycin solution (Irvine Scientific #9366).

A 96-well Adenylyl Cyclase Activation Flashplate™ was used (NEN: #SMP004A). First, 50ul of the standards for the assay were added to the plate, in duplicate, ranging from concentrations of 50pmol to zero pmol cAMP per well. The standard cAMP (NEN: #SMP004A) was reconstituted in water, and serial dilutions were made using 1xPBS (Irvine Scientific: #9240). Next, 50ul of the stimulation buffer (NEN: #SMP004A) was added to all wells. In the case of using compounds to measure activation or inactivation of cAMP, 10ul of each compound, diluted in water, was added to its respective well, in triplicate. Various final concentrations used range from 1uM up to 1mM. Adenosine 5'-triphosphate, ATP, (Research Biochemicals International: #A-141) and Adenosine 5'-diphosphate, ADP, (Sigma: #A2754) were used in the assay. Next, the 293 cells transfected with the respective cDNA (CMV or TDAG8) were harvested 24 (assay detection in serum media) or 48 hours post-transfection (assay detection comparing serum and serum-free media). The media was aspirated and the cells washed once with 1xPBS. Then 5ml of 1xPBS was added to the cells along with 3ml of cell dissociation buffer (Sigma: #C-1544). The detached cells were transferred to a centrifuge tube and centrifuged at room temperature for five minutes. The supernatant was removed and the cell pellet was resuspended in an appropriate amount of 1xPBS to obtain a final concentration of 2×10^6 cells per milliliter. To the wells containing the compound, 50ul of the cells in 1xPBS (1×10^5 cells/well) were added. The plate was incubated on a shaker for 15 minutes at room temperature. The detection buffer containing the tracer cAMP was prepared. In 11ml of detection buffer (NEN: #SMP004A), 50ul (equal to 1uCi) of [¹²⁵I]cAMP (NEN: #SMP004A) was added. Following incubation, 50ul of this detection buffer containing tracer cAMP was added to each well. The plate was placed on a shaker and

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incubated at room temperature for two hours. Finally, the solution from the wells of the plate were aspirated and the flashplate was counted using the Wallac MicroBeta™ scintillation counter.

In Figure 2A, ATP and ADP bind to endogenous TDAG8 resulting in an increase
5 of cAMP of about 59% and about 55% respectively. Figure 2B evidences ATP and ADP binding to endogenous TDAG8 where endogenous TDAG8 was transfected and grown in serum and serum-free medium. ATP binding to endogenous TDAG8 grown in serum media evidences an increase in cAMP of about 65%, compared to the endogenous TDAG8 with no compounds; in serum-free media there was an increase of about 68%. ADP
10 binding to endogenous TDAG8 in serum evidences about a 61% increase, while in serum-free ADP binding evidences an increase of about 62% increase. ATP and ADP bind to endogenous TDAG8 with an EC₅₀ value of 139.8uM and 120.5uM, respectively (data not shown).

Although the results presented in Figure 2B indicate substantially the same results
15 when serum and serum-free media were compared, our choice is to use a serum based media, although a serum-free media can also be utilized.

Example 6 **GPCR FUSION PROTEIN PREPARATION**

The design of the constitutively activated GPCR-G protein fusion construct was
20 accomplished as follows: both the 5' and 3' ends of the rat G protein G_sα (long form; Itoh, H. et al., 83 PNAS 3776 (1986)) were engineered to include a HindIII (5'-AAGCTT-3') sequence thereon. Following confirmation of the correct sequence (including the flanking HindIII sequences), the entire sequence was shuttled into pcDNA3.1(-) (Invitrogen, cat. no. V795-20) by subcloning using the HindIII restriction site of that vector. The correct

orientation for the G α sequence was determined after subcloning into pcDNA3.1(-). The modified pcDNA3.1(-) containing the rat G α gene at HindIII sequence was then verified; this vector was now available as a "universal" G α protein vector. The pcDNA3.1(-) vector contains a variety of well-known restriction sites upstream of the HindIII site, thus 5 beneficially providing the ability to insert, upstream of the G β protein, the coding sequence of an endogenous, constitutively active GPCR. This same approach can be utilized to create other "universal" G protein vectors, and, of course, other commercially available or proprietary vectors known to the artisan can be utilized – the important criteria is that the sequence for the GPCR be upstream and in-frame with that of the G protein.

10 TDAG8 couples via G α , while H9 couples via G γ . For the following exemplary GPCR Fusion Proteins, fusion to G α was accomplished.

A TDAG8(I225K)-G α Fusion Protein construct was made as follows: primers were designed as follows:

5'-gatcTCTAGAACAGCACATGTATTGAAG-3' (SEQ.ID.NO.: 125; sense)

15 5'-ctggGTACCCGCTCAAGGACCTCTAATTCCATAG-3' (SEQ.ID.NO.: 126; antisense).

Nucleotides in lower caps are included as spacers in the restriction sites between the G protein and TDAG8. The sense and anti-sense primers included the restriction sites for XbaI and KpnI, respectively.

PCR was then utilized to secure the respective receptor sequences for fusion within 20 the G α universal vector disclosed above, using the following protocol for each: 100ng cDNA for TDAG8 was added to separate tubes containing 2uL of each primer (sense and anti-sense), 3uL of 10mM dNTPs, 10uL of 10XTaqPlus™ Precision buffer, 1uL of TaqPlus™ Precision polymerase (Stratagene: #600211), and 80uL of water. Reaction temperatures and cycle times for TDAG8 were as follows: the initial denaturing step was done at 94 °C for five minutes, and

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a cycle of 94°C for 30 seconds; 55°C for 30 seconds; 72°C for two minutes. A final extension time was done at 72°C for ten minutes. PCR product for was run on a 1% agarose gel and then purified (data not shown). The purified product was digested with XbaI and KpnI (New England Biolabs) and the desired inserts purified and ligated into the Gs universal vector at the respective restriction site. The positive clones was isolated following transformation and determined by restriction enzyme digest; expression using 293 cells was accomplished following the protocol set forth *infra*. Each positive clone for TDAG8:Gs - Fusion Protein was sequenced to verify correctness.

10 GPCR Fusion Proteins comprising non-endogenous, constitutively activated TDAG8(I225K) were analyzed as above and verified for constitutive activation.

An H9(F236K)-G α Fusion Protein construct was made as follows: primers were designed as follows:

5'-TTAgatatacGGGGCCCACCCCTAGCGGT-3' (SEQ.ID.NO.: 145; sense)

5'-ggtaccCCCACAGCCATTCATCAGGATC-3' (SEQ.ID.NO.: 146; antisense).

15 Nucleotides in lower caps are included as spacers in the restriction sites between the G protein and H9. The sense and anti-sense primers included the restriction sites for EcoRV and KpnI, respectively such that spacers (attributed to the restriction sites) exists between the G protein and H9.

PCR was then utilized to secure the respective receptor sequences for fusion within 20 the G α universal vector disclosed above, using the following protocol for each: 80ng cDNA for H9 was added to separate tubes containing 100ng of each primer (sense and anti-sense), and 45uL of PCR Supermix™ (Gibco-Brl, LifeTech) (50ul total reaction volume). Reaction temperatures and cycle times for H9 were as follows: the initial denaturing step was done it 94°C for one, and a cycle of 94°C for 30 seconds; 55°C for 30 seconds; 72°C for two

minutes. A final extension time was done at 72°C for seven minutes. PCR product for was run on a 1% agarose gel and then purified (data not shown). The purified product was cloned into pCRII-TOPO™ System followed by identification of positive clones. Positive clones were isolated, digested with EcoRV and KpnI (New England Biolabs) and the desired inserts 5 were isolated, purified and ligated into the Gs universal vector at the respective restriction site. The positive clones was isolated following transformation and determined by restriction enzyme digest; expression using 293 cells was accomplished following the protocol set forth *infra*. Each positive clone for H9(F236K):Gs – Fusion Protein was sequenced to verify correctness. Membranes were frozen (-80°C) until utilized.

10 To ascertain the ability of measuring a cAMP response mediated by the Gs protein (even though H9 couples with Gz), the following cAMP membrane assay was utilized, based upon an NEN Adenyl Cyclase Activation Flahplate™ Assay kit (96 well format). "Binding Buffer" consisted of 10mM HEPES, 100mM NaCl and 10mM MgCl (ph 7.4). "Regeneration Buffer" was prepared in Binding Buffer and consisted of 20mM phosphocreatine, 20U 15 creatine phosphokinase, 20uM GTP, 0.2mM ATP, and 0.6mM IBMX. "cAMP Standards" were prepared in Binding Buffer as follows:

	cAMP Stock (5,000 pmol/ml in 2ml H ₂ O) in ul	Added to indicated amount of Binding Buffer	Final Assay Concentration (50ul into 100ul) to achieve indicated pmol/well
20	A 250	1ml	50
	B 500 of A	500ul	25
	C 500 of B	500ul	12.5
	D 500 of C	750ul	5.0
	E 500 of D	500ul	2.5
25	F 500 of E	500ul	1.25
	G 500 of F	750ul	0.5

Frozen membranes (both pCMV as control and the non-endogenous H(-Gs Fusion Protein) were thawed (on ice at room temperature until in solution). Membranes were

homogenized with a polytron until in suspension (2 x 15 seconds). Membrane protein concentration was determined using the Bradford Assay Protocol (*see infra*). Membrane concentration was diluted to 0.5mg/ml in Regeneration Buffer (final assay concentration – 25ug/well). Thereafter, 50ul of Binding Buffer was added to each well. For control, 50ul/well of cAMP standard was added to wells 11 and 12 A-G, with Binding Buffer alone to 12H (on the 96-well format). Thereafter, 50ul/well of protein was added to the wells and incubated at room temperature (on shaker) for 60min. 100ul [¹²⁵I]cAMP in Detection Buffer (*see infra*) was added to each well (final – 50ul [¹²⁵I]cAMP into 1ml Detection Buffer). These were incubated for 2hrs at room temperature. Plates were aspirated with an 8 channel manifold and sealed with plate covers. Results (pmoles cAMP bound) were read in a Wallac™ 1450 on "prot #15). Results are presented in Figure 3.

The results presented in Figure 3 indicate that the Gs coupled fusion was able to "drive" the cyclase reaction such that measurement of the constitutive activation of H9(F236K) was viable. Based upon these results, the direct identification of candidate compounds that are inverse agonists, agonists and partial agonists is possible using a cyclase-based assay.

Example 6

Protocol: Direct Identification of Inverse Agonists and Agonists Using [³⁵S]GTPγS

Although we have utilized endogenous, constitutively active GPCRs for the direct identification of candidate compounds as, e.g., inverse agonists, for reasons that are not altogether understood, intra-assay variation can become exacerbated. Preferably, then, a GPCR Fusion Protein, as disclosed above, is also utilized with a non-endogenous, constitutively activated GPCR. We have determined that when such a protein is used, intra-assay variation appears to be substantially stabilized, whereby an effective signal-to-noise ratio is obtained. This has the beneficial result of allowing for a more robust identification

of candidate compounds. Thus, it is preferred that for direct identification, a GPCR Fusion Protein be used and that when utilized, the following assay protocols be utilized.

Membrane Preparation

Membranes comprising the non-endogenous, constitutively active orphan GPCR Fusion Protein of interest and for use in the direct identification of candidate compounds as inverse agonists, agonists or partial agonists are preferably prepared as follows:

a. Materials

"Membrane Scrape Buffer" is comprised of 20mM HEPES and 10mM EDTA, pH 7.4; "Membrane Wash Buffer" is comprised of 20 mM HEPES and 0.1 mM EDTA, pH 7.4; "Binding Buffer" is comprised of 20mM HEPES, 100 mM NaCl, and 10 mM MgCl₂, pH 7.4

b. Procedure

All materials are kept on ice throughout the procedure. Firstly, the media is aspirated from a confluent monolayer of cells, followed by rinse with 10ml cold PBS, followed by aspiration. Thereafter, 5ml of Membrane Scrape Buffer is added to scrape cells; this is followed by transfer of cellular extract into 50ml centrifuge tubes (centrifuged at 20,000 rpm for 17 minutes at 4°C). Thereafter, the supernatant is aspirated and the pellet is resuspended in 30ml Membrane Wash Buffer followed by centrifuge at 20,000 rpm for 17 minutes at 4°C. The supernatant is then aspirated and the pellet resuspended in Binding Buffer. This is then homogenized using a Brinkman polytron™ homogenizer (15-20 second bursts until the all material is in suspension). This is referred to herein as "Membrane Protein".

Bradford Protein Assay

Following the homogenization, protein concentration of the membranes is determined using the Bradford Protein Assay (protein can be diluted to about 1.5mg/ml, aliquoted and

frozen (-80°C) for later use; when frozen, protocol for use is as follows: on the day of the assay, frozen Membrane Protein is thawed at room temperature, followed by vortex and then homogenized with a polytron at about 12 x 1,000 rpm for about 5-10 seconds; it is noted that for multiple preparations, the homogenizer should be thoroughly cleaned between 5 homogenization of different preparations).

a. Materials

Binding Buffer (as per above); Bradford Dye Reagent; Bradford Protein Standard are utilized, following manufacturer instructions (Biorad, cat. no. 500-0006).

b. Procedure

Duplicate tubes are prepared, one including the membrane, and one as a control "blank". Each contained 800ul Binding Buffer. Thereafter, 10ul of Bradford Protein Standard (1mg/ml) is added to each tube, and 10ul of membrane Protein is then added to just one tube (not the blank). Thereafter, 200ul of Bradford Dye Reagent is added to each tube, followed by vortex of each. After five (5) minutes, the tubes were re-vortexed and the material therein 15 is transferred to cuvettes. The cuvettes are then read using a CECIL 3041 spectrophotometer. at wavelength 595.

Direct Identification Assay

a. Materials

GDP Buffer consists of 37.5 ml Binding Buffer and 2mg GDP (Sigma, cat. no. G-20 7127), followed by a series of dilutions in Binding Buffer to obtain 0.2 uM GDP (final concentration of GDP in each well was 0.1 uM GDP); each well comprising a candidate compound, has a final volume of 200ul consisting of 100ul GDP Buffer (final concentration, 0.1uM GDP), 50ul Membrane Protein in Binding Buffer, and 50ul [³⁵S]GTPγS (0.6 nM) in

Binding Buffer (2.5 ul [³⁵S]GTP γ S per 10ml Binding Buffer).

b. Procedure

Candidate compounds are preferably screened using a 96-well plate format (these can be frozen at -80 °C). Membrane Protein (or membranes with expression vector excluding the 5 GPCR Fusion Protein, as control), are homogenized briefly until in suspension. Protein concentration is then determined using the Bradford Protein Assay set forth above. Membrane Protein (and control) is then diluted to 0.25mg/ml in Binding Buffer (final assay concentration, 12.5ug/well). Thereafter, 100 ul GDP Buffer is added to each well of a Wallac Scintistrip™ (Wallac). A 5ul pin-tool is then used to transfer 5 ul of a candidate compound 10 into such well (*i.e.*, 5ul in total assay volume of 200 ul is a 1:40 ratio such that the final screening concentration of the candidate compound is 10uM). Again, to avoid contamination, after each transfer step the pin tool should be rinsed in three reservoirs comprising water (1X), ethanol (1X) and water (2X) – excess liquid should be shaken from the tool after each rinse 15 and dried with paper and kimwipes. Thereafter, 50 ul of Membrane Protein is added to each well (a control well comprising membranes without the GPCR Fusion Protein is also utilized), and pre-incubated for 5-10 minutes at room temperature. Thereafter, 50 ul of [³⁵S]GTP γ S (0.6 nM) in Binding Buffer is added to each well, followed by incubation on a shaker for 60 minutes at room temperature (again, in this example, plates were covered with foil). The assay is then stopped by spinning of the plates at 4000 RPM for 15 minutes at 22 °C. The 20 plates are then aspirated with an 8 channel manifold and sealed with plate covers. The plates are then read on a Wallacc 1450 using setting "Prot. #37" (as per manufacturer instructions).

Example 7

Protocol: Confirmation Assay

Using an independent assay approach to provide confirmation of a directly identified

candidate compound as set forth above, it is preferred that a confirmation assay then be utilized. In this case, the preferred confirmation assay is a cyclase-based assay.

A modified Flash Plate™ Adenylyl Cyclase kit (New England Nuclear; Cat. No. SMP004A) is preferably utilized for confirmation of candidate compounds directly identified 5 as inverse agonists and agonists to non-endogenous, constitutively activated orphan GPCRs in accordance with the following protocol.

Transfected cells are harvested approximately three days after transfection. Membranes are prepared by homogenization of suspended cells in buffer containing 20mM HEPES, pH 7.4 and 10mM MgCl₂. Homogenization is performed on ice using a Brinkman 10 Polytron™ for approximately 10 seconds. The resulting homogenate is centrifuged at 49,000 X g for 15 minutes at 4°C. The resulting pellet is then resuspended in buffer containing 20mM HEPES, pH 7.4 and 0.1 mM EDTA, homogenized for 10 seconds, followed by centrifugation at 49,000 X g for 15 minutes at 4°C. The resulting pellet can be stored at - 15 80°C until utilized. On the day of direct identification screening, the membrane pellet is slowly thawed at room temperature, resuspended in buffer containing 20mM HEPES, pH 7.4 and 10mM MgCL2, to yield a final protein concentration of 0.60mg/ml (the resuspended membranes are placed on ice until use).

cAMP standards and Detection Buffer (comprising 2 µCi of tracer [¹²⁵I] cAMP (100 µl) to 11 ml Detection Buffer) are prepared and maintained in accordance with the 20 manufacturer's instructions. Assay Buffer is prepared fresh for screening and contained 20mM HEPES, pH 7.4, 10mM MgCl₂, 20mM phosphocreatine (Sigma), 0.1 units/ml creatine phosphokinase (Sigma), 50 µM GTP (Sigma), and 0.2 mM ATP (Sigma); Assay Buffer can be stored on ice until utilized.

Candidate compounds identified as per above (if frozen, thawed at room temperature) are added, preferably, to 96-well plate wells ($3\mu\text{l}/\text{well}$; $12\mu\text{M}$ final assay concentration), together with $40\mu\text{l}$ Membrane Protein ($30\mu\text{g}/\text{well}$) and $50\mu\text{l}$ of Assay Buffer. This admixture is then incubated for 30 minutes at room temperature, with gentle shaking.

5 Following the incubation, $100\mu\text{l}$ of Detection Buffer is added to each well, followed by incubation for 2-24 hours. Plates are then counted in a Wallac MicroBeta™ plate reader using "Prot. #31" (as per manufacturer instructions).

It is intended that each of the patents, applications, and printed publications mentioned in this patent document be hereby incorporated by reference in their entirety.

10 As those skilled in the art will appreciate, numerous changes and modifications may be made to the preferred embodiments of the invention without departing from the spirit of the invention. It is intended that all such variations fall within the scope of the invention.

15 Although a variety of expression vectors are available to those in the art, for purposes of utilization for both the endogenous and non-endogenous human GPCRs, it is most preferred that the vector utilized be pCMV. This vector was deposited with the American Type Culture Collection (ATCC) on October 13, 1998 (10801 University Blvd., Manassas, VA 20110-2209 USA) under the provisions of the Budapest Treaty for the International Recognition of the Deposit of Microorganisms for the Purpose of Patent Procedure. The DNA was tested by the ATCC and determined to be. The ATCC has 20 assigned the following deposit number to pCMV: ATCC #203351.

CLAIMS

What is claimed is:

1. A cDNA encoding a non-endogenous, constitutively activated version of a human G protein-coupled receptor comprising hARE-3(F313K).
- 5 2. A non-endogenous version of a human G protein-coupled receptor encoded by the cDNA of claim 1.
3. A Plasmid comprising a Vector and the cDNA of claim 1.
4. A Host Cell comprising the Plasmid of claim 3.
5. A cDNA encoding a non-endogenous, constitutively activated version of a human G protein-coupled receptor comprising hARE-4(V233K)
- 10 6. A non-endogenous version of a human G protein-coupled receptor encoded by the cDNA of claim 5.
7. A Plasmid comprising a Vector and the cDNA of claim 5.
8. A Host Cell comprising the Plasmid of claim 7.
- 15 9. A cDNA encoding a non-endogenous, constitutively activated version of a human G protein-coupled receptor comprising hARE-5(A240K).
10. A non-endogenous version of a human G protein-coupled receptor encoded by the cDNA of claim 9.
11. A Plasmid comprising a Vector and the cDNA of claim 5.
- 20 12. A Host Cell comprising the Plasmid of claim 11.
13. A cDNA encoding a non-endogenous, constitutively activated version of a human G protein-coupled receptor comprising hGPCR14(L257K).

14. A non-endogenous version of a human G protein-coupled receptor encoded by the cDNA of claim 13.
15. A Plasmid comprising a Vector and the cDNA of claim 13.
- 5 16. A Host Cell comprising the Plasmid of claim 15.
17. A cDNA encoding a non-endogenous, constitutively activated version of a human G protein-coupled receptor comprising hGPCR27(C283K).
18. A non-endogenous version of a human G protein-coupled receptor encoded by the cDNA of claim 17.
- 10 19. A Plasmid comprising a Vector and the cDNA of claim 17.
20. A Host Cell comprising the Plasmid of claim 19.
21. A cDNA encoding a non-endogenous, constitutively activated version of a human G protein-coupled receptor comprising hARE-1(E232K).
22. A non-endogenous version of a human G protein-coupled receptor encoded by the
15 cDNA of claim 21.
23. A Plasmid comprising a Vector and the cDNA of claim 21.
24. A Host Cell comprising the Plasmid of claim 23.
25. A cDNA encoding a non-endogenous, constitutively activated version of a human G protein-coupled receptor comprising hARE-2(G285K).
- 20 26. A non-endogenous version of a human G protein-coupled receptor encoded by the cDNA of claim 25.
27. A Plasmid comprising a Vector and the cDNA of claim 25.
28. A Host Cell comprising the Plasmid of claim 27.

29. A cDNA encoding a non-endogenous, constitutively activated version of a human G protein-coupled receptor comprising hPPR1(L239K).
30. A non-endogenous version of a human G protein-coupled receptor encoded by the cDNA of claim 29.
- 5 31. A Plasmid comprising a Vector and the cDNA of claim 29.
32. A Host Cell comprising the Plasmid of claim 31.
33. A cDNA encoding a non-endogenous, constitutively activated version of a human G protein-coupled receptor comprising hG2A(K232A).
34. A non-endogenous version of a human G protein-coupled receptor encoded by the cDNA of claim 33.
- 10 35. A Plasmid comprising a Vector and the cDNA of claim 33.
36. A Host Cell comprising the Plasmid of claim 35.
37. A cDNA encoding a non-endogenous, constitutively activated version of a human G protein-coupled receptor comprising hRUP3(L224K).
- 15 38. A non-endogenous version of a human G protein-coupled receptor encoded by the cDNA of claim 37.
39. A Plasmid comprising a Vector and the cDNA of claim 37.
40. A Host Cell comprising the Plasmid of claim 39.
41. A cDNA encoding a non-endogenous, constitutively activated version of a human G protein-coupled receptor comprising hRUP5(A236K).
- 20 42. A non-endogenous version of a human G protein-coupled receptor encoded by the cDNA of claim 41.
43. A Plasmid comprising a Vector and the cDNA of claim 41.

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44. A Host Cell comprising the Plasmid of claim 42.
45. A cDNA encoding a non-endogenous, constitutively activated version of a human G protein-coupled receptor comprising hRUP6(N267K)
46. A non-endogenous version of a human G protein-coupled receptor encoded by the
5 cDNA of claim 45.
47. A Plasmid comprising a Vector and the cDNA of claim 45.
48. A Host Cell comprising the Plasmid of claim 47.
49. A cDNA encoding a non-endogenous, constitutively activated version of a human G protein-coupled receptor comprising hRUP7(A302K).
- 10 50. A non-endogenous version of a human G protein-coupled receptor encoded by the cDNA of claim 49.
51. A Plasmid comprising a Vector and the cDNA of claim 49.
52. A Host Cell comprising the Plasmid of claim 51.
53. A cDNA encoding a non-endogenous, constitutively activated version of a human
15 G protein-coupled receptor comprising hCHN4(V236K).
54. A non-endogenous version of a human G protein-coupled receptor encoded by the cDNA of claim 53.
55. A Plasmid comprising a Vector and the cDNA of claim 53.
56. A Host Cell comprising the Plasmid of claim 55.
- 20 57. A cDNA encoding a non-endogenous, constitutively activated version of a human G protein-coupled receptor comprising hMC4(A244K).
58. A non-endogenous version of a human G protein-coupled receptor encoded by the cDNA of claim 57.

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59. A Plasmid comprising a Vector and the cDNA of claim 57.
60. A Host Cell comprising the Plasmid of claim 60.
61. A cDNA encoding a non-endogenous, constitutively activated version of a human G protein-coupled receptor comprising hCHN3(S284K).
- 5 62. A non-endogenous version of a human G protein-coupled receptor encoded by the cDNA of claim 61.
63. A Plasmid comprising a Vector and the cDNA of claim 61.
64. A Host Cell comprising the Plasmid of claim 63.
65. A cDNA encoding a non-endogenous, constitutively activated version of a human G protein-coupled receptor comprising hCHN6(L352K).
- 10 66. A non-endogenous version of a human G protein-coupled receptor encoded by the cDNA of claim 65.
67. A Plasmid comprising a Vector and the cDNA of claim 65.
68. A Host Cell comprising the Plasmid of claim 67.
- 15 69. A cDNA encoding a non-endogenous, constitutively activated version of a human G protein-coupled receptor comprising hCHN8(N235K).
70. A non-endogenous version of a human G protein-coupled receptor encoded by the cDNA of claim 69.
71. A Plasmid comprising a Vector and the cDNA of claim 69.
- 20 72. A Host Cell comprising the Plasmid of claim 71.
73. A cDNA encoding a non-endogenous, constitutively activated version of a human G protein-coupled receptor comprising hH9(F236K).
74. A non-endogenous version of a human G protein-coupled receptor encoded by the

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cDNA of claim 73.

75. A Plasmid comprising a Vector and the cDNA of claim 73.

76. A Host Cell comprising the Plasmid of claim 74.

77. A cDNA encoding a non-endogenous, constitutively activated version of a human

5 G protein-coupled AT1 receptor selected from the group consisting of:

hAT1(F239K); hAT1(N111A); hAT1(AT2K255IC3); and hAT1(A243+).

78. A non-endogenous version of a human G protein-coupled receptor encoded by a
cDNA of claim 77.

79. A Plasmid comprising a Vector and the cDNA of claim 77.

10 80. A Host Cell comprising the Plasmid of claim 79.

1 / 2

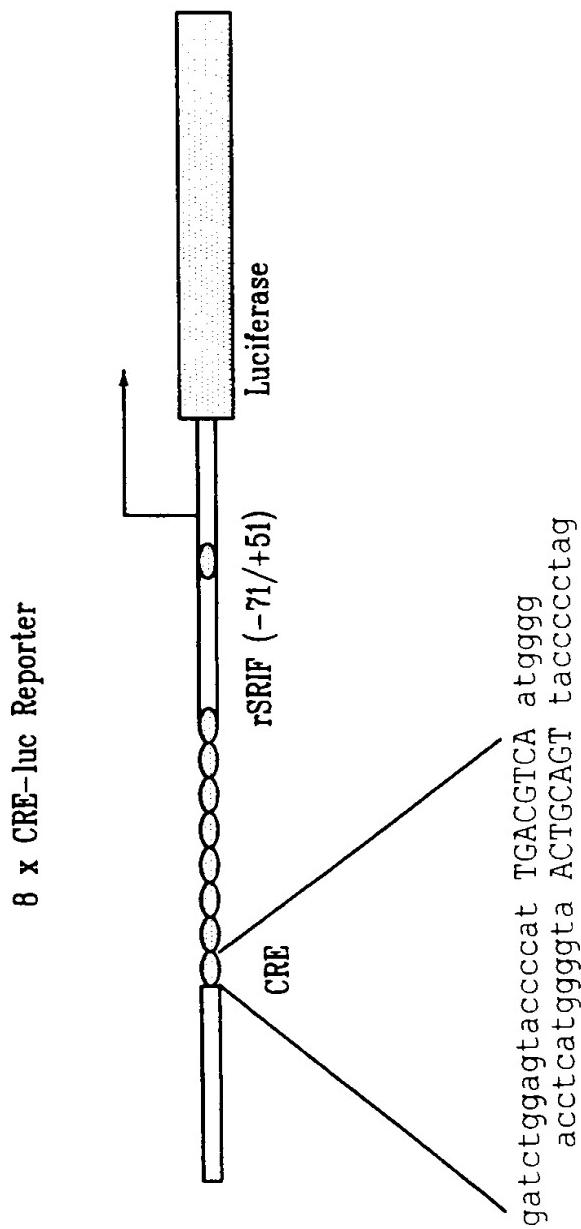


FIG. 1

2/2

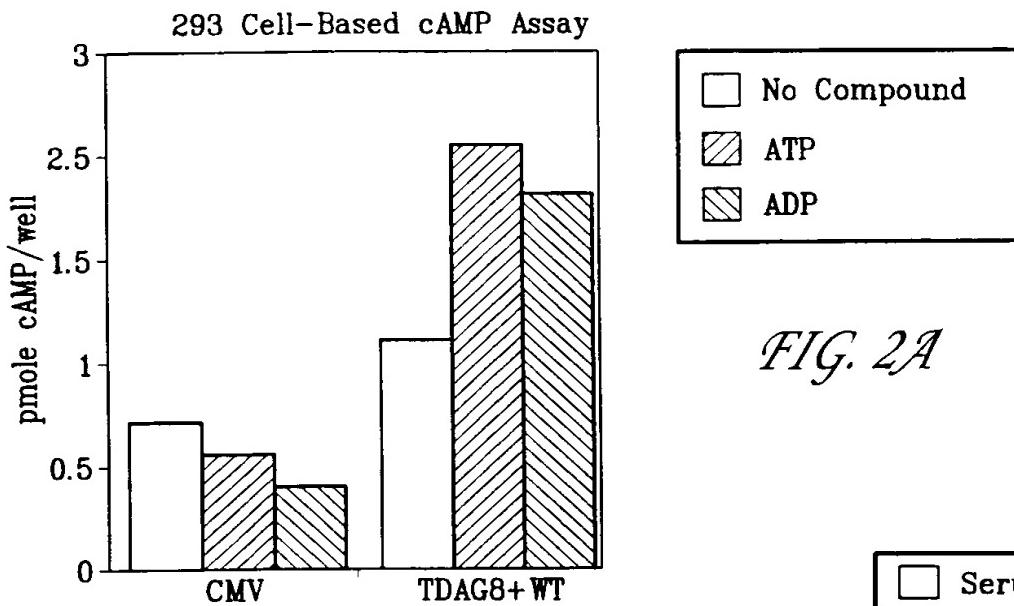


FIG. 2A

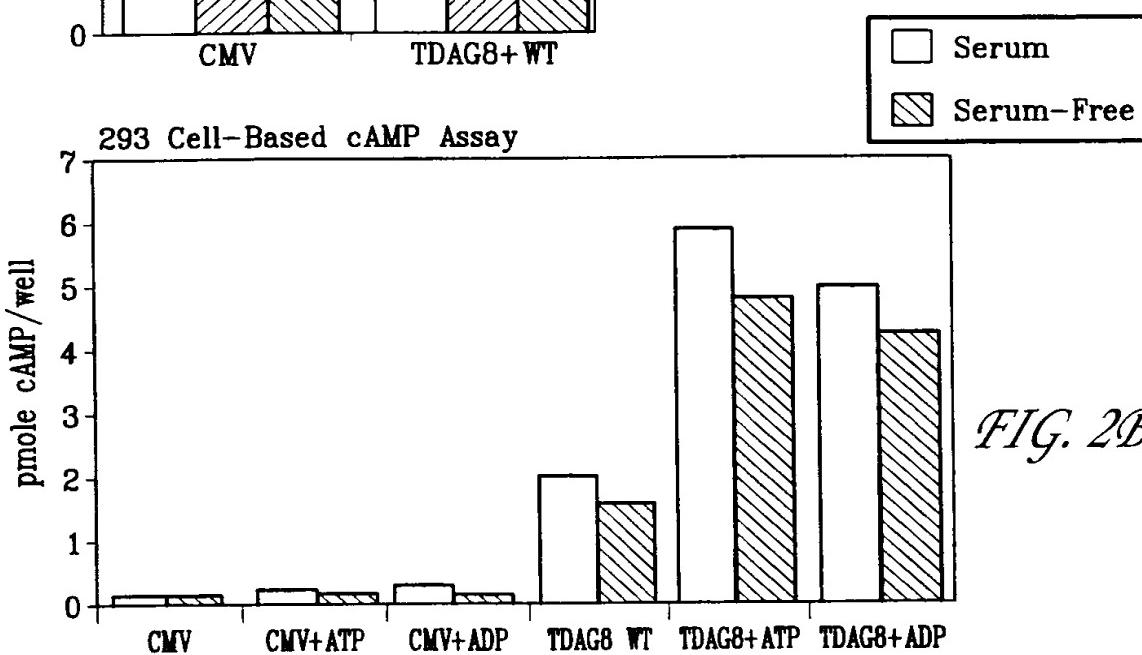


FIG. 2B

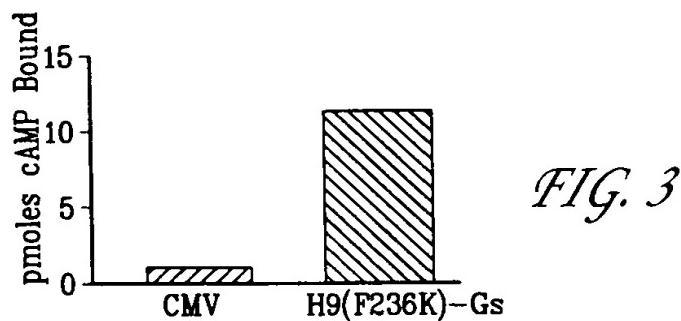


FIG. 3

- 1 -

SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: Behan, Dominic P.
5 Lehmann-Bruinsma, Karin
Chalmers, Derek T.
Lowitz, Kevin P.
Lin, I-Lin
Dang, Huong T.
10 Chen, Ruoping
Liaw, Chen W.
Gore, Martin J.
White, Carol
- (ii) TITLE OF INVENTION: Non-Endogenous, Constitutively Activated Human G
15 Protein-Coupled Receptors
- (iii) NUMBER OF SEQUENCES: 146
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- 25 (v) COMPUTER READABLE FORM:
(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.30
- 30 (vi) CURRENT APPLICATION DATA:
(A) APPLICATION NUMBER: US
(B) FILING DATE:
(C) CLASSIFICATION:
- (viii) ATTORNEY/AGENT INFORMATION:
35 (A) NAME: Burgoon, Richard P.
(B) REGISTRATION NUMBER: 34,787
- (ix) TELECOMMUNICATION INFORMATION:
(A) TELEPHONE: (858) 453-7200
(B) TELEFAX: (858) 453-7210
- 40 (2) INFORMATION FOR SEQ ID NO:1:
- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1260 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single

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(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

	ATGGTCTTCT CGGCAGTGTT GACTGCGTTC CATAACGGGA CATCCAACAC AACATTTGTC	60
5	GTTGATGAAA ACACCTACAT GAATATTACA CTCCCTCCAC CATTCCAGCA TCCTGACCTC	120
	AGTCCATTGC TTAGATATAG TTTTGAAACC ATGGCTCCC CTGGTTGAG TTCCTTGACC	180
	GTGAATAGTA CAGCTGTGCC CACAACACCA GCAGCATTAA AGAGCCTAAA CTTGCCTCTT	240
	CAGATCACCC TTTCTGCTAT AATGATATTTC ATTCTGTTTG TGTCTTTCT TGGAACATTG	300
	GTTGTTGCC TCATGGTTA CAAAAAAGCT GCCATGAGGT CTGCAATTAA CATCCTCCTT	360
10	GCCAGCCTAG CTTTGAGA CATGTTGCTT GCAGTGCTGA ACATGCCCTT TGCCCTGGTA	420
	ACTATTCTTA CTACCCGATG GATTTTGAGG AAATTCTTCT GTAGGGTATC TGCTATGTTT	480
	TTCTGGTTAT TTGTGATAGA AGGAGTAGCC ATCCTGCTCA TCATTAGCAT AGATAGGTT	540
	CTTATTATAG TCCAGAGGCA GGATAAGCTA AACCCATATA GAGCTAAGGT TCTGATTGCA	600
	GTTCTTGGG CAACTCCTT TTGTGAGCT TTTCTTTAG CCGTAGGAAA CCCGACCTG	660
15	CAGATACCTT CCCGAGCTCC CCAGTGTGTG TTTGGGTACA CAACCAATCC AGGCTACCAG	720
	GCTTATGTGA TTTGATTTC TCTCATTCTT TTCTTCATAC CCTTCCTGGT AATACTGTAC	780
	TCATTTATGG GCATACTCAA CACCCTTCGG CACAATGCCT TGAGGATCCA TAGCTACCCT	840
	GAAGGTATAT GCCTCAGCCA GGCCAGCAA CTGGGTCTCA TGAGTCTGCA GAGACCTTTC	900
	CAGATGAGCA TTGACATGGG CTTTAAAACA CGTGCCTTCA CCACTATTTT GATTCTCTT	960
20	GCTGTCTTCA TTGTCTGCTG GGCCCCATTC ACCACTTACA GCCTTGTGGC AACATTCACT	1020
	AAGCACTTTT ACTATCAGCA CAACTTTTT GAGATTAGCA CCTGGCTACT GTGGCTCTGC	1080
	TACCTCAAGT CTGCATTGAA TCCGCTGATC TACTACTGGA GGATTAAGAA ATTCCATGAT	1140
	GCTTGCCTGG ACATGATGCC TAAGTCCTTC AAGTTTTGC CGCAGCTCCC TGGTCACACA	1200
	AAGCGACGGA TACGTCCCTAG TGCTGTCTAT GTGTGTGGGG AACATCGGAC GGTGGTGTGA	1260

25 (3) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 419 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

30

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(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

	Met Val Phe Ser Ala Val Leu Thr Ala Phe His Thr Gly Thr Ser Asn				
1	5	10	15		
5	Thr Thr Phe Val Val Tyr Glu Asn Thr Tyr Met Asn Ile Thr Leu Pro	20	25	30	
	Pro Pro Phe Gln His Pro Asp Leu Ser Pro Leu Leu Arg Tyr Ser Phe	35	40	45	
10	Glu Thr Met Ala Pro Thr Gly Leu Ser Ser Leu Thr Val Asn Ser Thr	50	55	60	
	Ala Val Pro Thr Thr Pro Ala Ala Phe Lys Ser Leu Asn Leu Pro Leu	65	70	75	80
	Gln Ile Thr Leu Ser Ala Ile Met Ile Phe Ile Leu Phe Val Ser Phe	85	90	95	
15	Leu Gly Asn Leu Val Val Cys Leu Met Val Tyr Gln Lys Ala Ala Met	100	105	110	
	Arg Ser Ala Ile Asn Ile Leu Leu Ala Ser Leu Ala Phe Ala Asp Met	115	120	125	
20	Leu Leu Ala Val Leu Asn Met Pro Phe Ala Leu Val Thr Ile Leu Thr	130	135	140	
	Thr Arg Trp Ile Phe Gly Lys Phe Cys Arg Val Ser Ala Met Phe	145	150	155	160
	Phe Trp Leu Phe Val Ile Glu Gly Val Ala Ile Leu Leu Ile Ile Ser	165	170	175	
25	Ile Asp Arg Phe Leu Ile Ile Val Gln Arg Gln Asp Lys Leu Asn Pro	180	185	190	
	Tyr Arg Ala Lys Val Leu Ile Ala Val Ser Trp Ala Thr Ser Phe Cys	195	200	205	
30	Val Ala Phe Pro Leu Ala Val Gly Asn Pro Asp Leu Gln Ile Pro Ser	210	215	220	
	Arg Ala Pro Gln Cys Val Phe Gly Tyr Thr Thr Asn Pro Gly Tyr Gln	225	230	235	240
	Ala Tyr Val Ile Leu Ile Ser Leu Ile Ser Phe Phe Ile Pro Phe Leu	245	250	255	
35	Val Ile Leu Tyr Ser Phe Met Gly Ile Leu Asn Thr Leu Arg His Asn	260	265	270	

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	Ala Leu Arg Ile His Ser Tyr Pro Glu Gly Ile Cys Leu Ser Gln Ala			
	275	280	285	
	Ser Lys Leu Gly Leu Met Ser Leu Gln Arg Pro Phe Gln Met Ser Ile			
	290	295	300	
5	Asp Met Gly Phe Lys Thr Arg Ala Phe Thr Thr Ile Leu Ile Leu Phe			
	305	310	315	320
	Ala Val Phe Ile Val Cys Trp Ala Pro Phe Thr Thr Tyr Ser Leu Val			
	325	330	335	
10	Ala Thr Phe Ser Lys His Phe Tyr Tyr Gln His Asn Phe Phe Glu Ile			
	340	345	350	
	Ser Thr Trp Leu Leu Trp Leu Cys Tyr Leu Lys Ser Ala Leu Asn Pro			
	355	360	365	
	Leu Ile Tyr Tyr Trp Arg Ile Lys Lys Phe His Asp Ala Cys Leu Asp			
	370	375	380	
15	Met Met Pro Lys Ser Phe Lys Phe Leu Pro Gln Leu Pro Gly His Thr			
	385	390	395	400
	Lys Arg Arg Ile Arg Pro Ser Ala Val Tyr Val Cys Gly Glu His Arg			
	405	410	415	
20	Thr Val Val			

(4) INFORMATION FOR SEQ ID NO:3:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1119 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

ATGTTAGCCA ACAGCTCCTC AACCAACAGT TCTGTTCTCC CGTGTCTGA CTACCGACCT	60
30 ACCCACCGCC TGCACTTGGT GGTCTACAGC TTGGTGCTGG CTGCCGGGCT CCCCTCAAC	120
GCGCTAGCCC TCTGGGTCTT CCTGCGCGCG CTGCGCGTGC ACTCGGTGGT GAGCGTGTAC	180
ATGTGTAACC TGGCGGCCAG CGACCTGCTC TTCACCCCTCT CGCTGCCCGT TCGTCTCTCC	240
TACTACGCAC TGCACCACTG GCCCTTCCCC GACCTCCTGT GCCAGACGAC GGGCGCCATC	300
TTCCAGATGA ACATGTACGG CAGCTGCATC TTCCTGATGC TCATCAACGT GGACCGCTAC	360

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GCCGCCATCG	TGCACCCGCT	GCGACTGCGC	CACCTGCGGC	GGCCCCGCGT	GGCGCGGCTG	420
CTCTGCCTGG	GCGTGTGGC	GCTCATCCTG	GTGTTGCCG	TGCCC GCCGC	CCGCGTGCAC	480
AGGCCCTCGC	GTTGCCGCTA	CCGGGACCTC	GAGGTGCGCC	TATGCTTCGA	GAGCTTCAGC	540
GACGAGCTGT	GGAAAGGCAG	GCTGCTGCC	CTCGTGTGC	TGGCCGAGGC	GCTGGGCTTC	600
5 CTGCTGCC	TGGCGCGGT	GGTCTACTCG	TCGGGCCGAG	TCTTCTGGAC	GCTGGCGCGC	660
CCCGACGCCA	CGCAGAGCCA	GCGGCCGGCGG	AAGACCGTGC	GCCTCCTGCT	GGCTAACCTC	720
GTCATCTTCC	TGCTGTGCTT	CGTGCCCTAC	AACAGCACGC	TGGCGGTCTA	CGGGCTGCTG	780
CGGAGCAAGC	TGGTGGCGGC	CAGCGTGCCT	GCCCGCGATC	GCGTGC CGGG	GGTGCTGATG	840
GTGATGGTGC	TGCTGGCCGG	CGCCA ACTGC	GTGCTGGACC	CGCTGGTGT	CTACTTTAGC	900
10 GCCGAGGGCT	TCCGCAACAC	CCTGCCGCGC	CTGGGCACTC	CGCACCGGGC	CAGGACCTCG	960
GCCACCAACG	GGACGCGGGC	GGCGCTCGCG	CAATCCGAAA	GGTCCGCCGT	CACCACCGAC	1020
GCCACCCAGGC	CGGATGCCGC	CAGTCAGGGG	CTGCTCCGAC	CCTCCGACTC	CCACTCTCTG	1080
TCTTCCTTCA	CACAGTGTCC	CCAGGATTCC	GCCCTCTGA			1119

(5) INFORMATION FOR SEQ ID NO:4:

15 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 372 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: not relevant

20 (ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Met	Leu	Ala	Asn	Ser	Ser	Ser	Thr	Asn	Ser	Ser	Val	Leu	Pro	Cys	Pro
1				5					10			15			
Asp	Tyr	Arg	Pro	Thr	His	Arg	Leu	His	Leu	Val	Val	Tyr	Ser	Leu	Val
25				20				25				30			
Leu	Ala	Ala	Gly	Leu	Pro	Leu	Asn	Ala	Leu	Ala	Leu	Trp	Val	Phe	Leu
				35				40				45			
Arg	Ala	Leu	Arg	Val	His	Ser	Val	Val	Ser	Val	Tyr	Met	Cys	Asn	Leu
				50				55			60				
30 Ala	Ala	Ser	Asp	Leu	Leu	Phe	Thr	Leu	Ser	Leu	Pro	Val	Arg	Leu	Ser
				65				70			75				80
Tyr	Tyr	Ala	Leu	His	His	Trp	Pro	Phe	Pro	Asp	Leu	Leu	Cys	Gln	Thr

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	85	90	95
	Thr Gly Ala Ile Phe Gln Met Asn Met Tyr Gly Ser Cys Ile Phe Leu		
	100	105	110
5	Met Leu Ile Asn Val Asp Arg Tyr Ala Ala Ile Val His Pro Leu Arg		
	115	120	125
	Leu Arg His Leu Arg Arg Pro Arg Val Ala Arg Leu Leu Cys Leu Gly		
	130	135	140
	Val Trp Ala Leu Ile Leu Val Phe Ala Val Pro Ala Ala Arg Val His		
10	145	150	155
	Arg Pro Ser Arg Cys Arg Tyr Arg Asp Leu Glu Val Arg Leu Cys Phe		
	165	170	175
	Glu Ser Phe Ser Asp Glu Leu Trp Lys Gly Arg Leu Leu Pro Leu Val		
	180	185	190
15	Leu Leu Ala Glu Ala Leu Gly Phe Leu Leu Pro Leu Ala Ala Val Val		
	195	200	205
	Tyr Ser Ser Gly Arg Val Phe Trp Thr Leu Ala Arg Pro Asp Ala Thr		
	210	215	220
	Gln Ser Gln Arg Arg Lys Thr Val Arg Leu Leu Leu Ala Asn Leu		
	225	230	235
20	Val Ile Phe Leu Leu Cys Phe Val Pro Tyr Asn Ser Thr Leu Ala Val		
	245	250	255
	Tyr Gly Leu Leu Arg Ser Lys Leu Val Ala Ala Ser Val Pro Ala Arg		
	260	265	270
25	Asp Arg Val Arg Gly Val Leu Met Val Met Val Leu Leu Ala Gly Ala		
	275	280	285
	Asn Cys Val Leu Asp Pro Leu Val Tyr Tyr Phe Ser Ala Glu Gly Phe		
	290	295	300
	Arg Asn Thr Leu Arg Gly Leu Gly Thr Pro His Arg Ala Arg Thr Ser		
	305	310	315
30	Ala Thr Asn Gly Thr Arg Ala Ala Leu Ala Gln Ser Glu Arg Ser Ala		
	325	330	335
	Val Thr Thr Asp Ala Thr Arg Pro Asp Ala Ala Ser Gln Gly Leu Leu		
	340	345	350
35	Arg Pro Ser Asp Ser His Ser Leu Ser Ser Phe Thr Gln Cys Pro Gln		
	355	360	365
	Asp Ser Ala Leu		
	370		

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(6) INFORMATION FOR SEQ ID NO:5:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1107 base pairs
 - (B) TYPE: nucleic acid
 - 5 (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

	ATGGCCAACCT CCACAGGGCT GAACGCCTCA GAAGTCGCAG GCTCGTTGGG GTTGATCCTG	60
10	GCAGCTGTCG TGGAGGTGGG GGCACTGCTG GGCAACGGCG CGCTGCTGGT CGTGGTGCTG	120
	CGCACGCCGG GACTGCGCGA CGCGCTCTAC CTGGCGCACC TGTGCGTCGT GGACCTGCTG	180
	GCGGCCGCCT CCATCATGCC GCTGGGCCTG CTGGCCGCAC CGCCGCCCGG GCTGGGCCGC	240
	GTGCGCCTGG GCCCCGCGCC ATGCCGCGCC GCTCGCTTCC TCTCCGCCGC TCTGCTGCCG	300
	GCCTGCACGC TCGGGGTGGC CGCACTTGGC CTGGCACGCT ACCGCCTCAT CGTGCACCCG	360
15	CTGCGGCCAG GCTCGCGGCC GCCGCCTGTG CTCGTGCTCA CCGCCGTGTG GGCCGCGGCG	420
	GGACTGCTGG GCGCGCTCTC CCTGCTCGGC CCGCCGCCCG CACCGCCCCC TGCTCCTGCT	480
	CGCTGCTCGG TCCTGGCTGG GGGCCTCGGG CCCTTCCGGC CGCTCTGGC CCTGCTGGCC	540
	TTCGCGCTGC CCGCCCTCCT GCTGCTCGGC GCCTACGGCG GCATCTTCGT GGTGGCGCGT	600
	CGCGCTGCC CGAGGCCCCC ACGGCCGGCG CGCGGGTCCC GACTCCGCTC GGACTCTCTG	660
20	GATAGCCGCC TTTCCATCTT GCCGCCGCTC CGGCCTCGCC TGCCCGGGGG CAAGGCGGCC	720
	CTGGCCCCAG CGCTGGCCGT GGGCAATTG GCAGCCTGCT GGCTGCCTTA TGGCTGCGCC	780
	TGCCTGGCGC CCGCAGCGCG GGCCGCGGAA GCCGAAGCGG CTGTCACCTG GGTCGCCTAC	840
	TCGGCCTTCG CGGCTCACCC CTTCCGTAC GGGCTGCTGC AGCGCCCCGT GCGCTTGGCA	900
	CTGGGCCGCC TCTCTCGCCG TGCACTGCTT GGACCTGTGC GGGCCTGCAC TCCGCAAGCC	960
25	TGGCACCCGC GGGCACTCTT GCAATGCCTC CAGAGACCCC CAGAGGGCCC TGCCGTAGGC	1020
	CCTTCTGAGG CTCCAGAAC A GACCCCCGAG TTGGCAGGAG GGCGGAGCCC CGCATACCAAG	1080
	GGGCCACCTG AGAGTTCTCT CTCCTGA	1107

(7) INFORMATION FOR SEQ ID NO:6:

- 30 (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 368 amino acids

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- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: protein

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Met Ala Asn Ser Thr Gly Leu Asn Ala Ser Glu Val Ala Gly Ser Leu
1 5 10 15

Gly Leu Ile Leu Ala Ala Val Val Glu Val Gly Ala Leu Leu Gly Asn
20 25 30

10 Gly Ala Leu Leu Val Val Val Leu Arg Thr Pro Gly Leu Arg Asp Ala
35 40 45

Leu Tyr Leu Ala His Leu Cys Val Val Asp Leu Leu Ala Ala Ser
50 55 60

15 Ile Met Pro Leu Gly Leu Leu Ala Ala Pro Pro Pro Gly Leu Gly Arg
65 70 75 80

Val Arg Leu Gly Pro Ala Pro Cys Arg Ala Ala Arg Phe Leu Ser Ala
85 90 95

Ala Leu Leu Pro Ala Cys Thr Leu Gly Val Ala Ala Leu Gly Leu Ala
100 105 110

20 Arg Tyr Arg Leu Ile Val His Pro Leu Arg Pro Gly Ser Arg Pro Pro
115 120 125

Pro Val Leu Val Leu Thr Ala Val Trp Ala Ala Gly Leu Leu Gly
130 135 140

25 Ala Leu Ser Leu Leu Gly Pro Pro Pro Ala Pro Pro Pro Ala Pro Ala
145 150 155 160

Arg Cys Ser Val Leu Ala Gly Gly Leu Gly Pro Phe Arg Pro Leu Trp
165 170 175

Ala Leu Leu Ala Phe Ala Leu Pro Ala Leu Leu Leu Gly Ala Tyr
180 185 190

30 Gly Gly Ile Phe Val Val Ala Arg Arg Ala Ala Leu Arg Pro Pro Arg
195 200 205

Pro Ala Arg Gly Ser Arg Leu Arg Ser Asp Ser Leu Asp Ser Arg Leu
210 215 220

35 Ser Ile Leu Pro Pro Leu Arg Pro Arg Leu Pro Gly Gly Lys Ala Ala
225 230 235 240

Leu Ala Pro Ala Leu Ala Val Gly Gln Phe Ala Ala Cys Trp Leu Pro

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	245	250	255
	Tyr Gly Cys Ala Cys Leu Ala Pro Ala Ala Arg Ala Ala Glu Ala Glu		
	260	265	270
5	Ala Ala Val Thr Trp Val Ala Tyr Ser Ala Phe Ala Ala His Pro Phe		
	275	280	285
	Leu Tyr Gly Leu Leu Gln Arg Pro Val Arg Leu Ala Leu Gly Arg Leu		
	290	295	300
10	Ser Arg Arg Ala Leu Pro Gly Pro Val Arg Ala Cys Thr Pro Gln Ala		
	305	310	315
	Trp His Pro Arg Ala Leu Leu Gln Cys Leu Gln Arg Pro Pro Glu Gly		
	325	330	335
	Pro Ala Val Gly Pro Ser Glu Ala Pro Glu Gln Thr Pro Glu Leu Ala		
	340	345	350
15	Gly Gly Arg Ser Pro Ala Tyr Gln Gly Pro Pro Glu Ser Ser Leu Ser		
	355	360	365

(8) INFORMATION FOR SEQ ID NO:7:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1008 base pairs
 - (B) TYPE: nucleic acid
 - 20 (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

	ATGGAATCAT CTTTCTCATT TGGAGTGATC CTTGCTGTCC TGGCCTCCCT CATCATTGCT	60
25	ACTAACACAC TAGTGGCTGT GGCTGTGCTG CTGTTGATCC ACAAGAATGA TGGTGTCACT	120
	CTCTGCTTCA CCTTGAATCT GGCTGTGGCT GACACCTTGA TTGGTGTGGC CATCTCTGGC	180
	CTACTCACAG ACCAGCTCTC CAGCCCTTCT CGGCCACAC AGAAGACCCT GTGCAGCCTG	240
	CGGATGGCAT TTGTCACTTC CTCCGCAGCT GCCTCTGTCC TCACGGTCAT GCTGATCACC	300
	TTTGACAGGT ACCTTGCCAT CAAGCAGCCC TTCCGCTACT TGAAGATCAT GAGTGGTTC	360
30	GTGGCCGGGG CCTGCATTGC CGGGCTGTGG TTAGTGTCTT ACCTCATTGG CTTCCCTCCA	420
	CTCGGAATCC CCATGTTCCA GCAGACTGCC TACAAAGGGC AGTGCAGCTT CTTTGCTGTA	480
	TTTCACCCCTC ACTTCGTGCT GACCCTCTCC TGCCTGGCT TCTTCCCAGC CATGCTCCTC	540
	TTTGTCTTCT TCTACTGCGA CATGCTCAAG ATTGCCTCCA TGCACAGCCA GCAGATTGCA	600

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AAGATGGAAC	ATGCAGGAGC	CATGGCTGGA	GGTTATCGAT	CCCCACGGAC	TCCCAGCGAC	660
TTCAAAGCTC	TCCGTACTGT	GTCTGTTCTC	ATTGGGAGCT	TTGCTCTATC	CTGGACCCCC	720
TTCCTTATCA	CTGGCATTGT	GCAGGTGGCC	TGCCAGGAGT	GTCACCTCTA	CCTAGTGCTG	780
GAACGGTACC	TGTGGCTGCT	CGGCGTGGGC	AACTCCCTGC	TCAACCCACT	CATCTATGCC	840
5 TATTGGCAGA	AGGAGGTGCG	ACTGCAGCTC	TACCACATGG	CCCTAGGAGT	GAAGAAGGTG	900
CTCACCTCAT	TCCTCCTCTT	TCTCTCGGCC	AGGAATTGTG	GCCCAGAGAG	GCCCAGGGAA	960
AGTTCCGTGTC	ACATCGTCAC	TATCTCCAGC	TCAGAGTTG	ATGGCTAA		1008

(9) INFORMATION FOR SEO ID NO: 8:

- 10 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 335 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: not relevant

- (ii) MOLECULE TYPE: protein

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Met Glu Ser Ser Phe Ser Phe Gly Val Ile Leu Ala Val Leu Ala Ser
 1 5 10 15

Leu Ile Ile Ala Thr Asn Thr Leu Val Ala Val Ala Val Leu Leu Leu
20 25 30

20 Ile His Lys Asn Asp Gly Val Ser Leu Cys Phe Thr Leu Asn Leu Ala
35 40 45

Val Ala Asp Thr Leu Ile Gly Val Ala Ile Ser Gly Leu Leu Thr Asp
50 55 60

25 Gln Leu Ser Ser Pro Ser Arg Pro Thr Gln Lys Thr Leu Cys Ser Leu
65 70 75 80

Arg Met Ala Phe Val Thr Ser Ser Ala Ala Ala Ser Val Leu Thr Val
85 90 95

Met	Leu	Ile	Thr	Phe	Asp	Arg	Tyr	Leu	Ala	Ile	Lys	Gln	Pro	Phe	Arg
				100					105					110	

Tyr Leu Lys Ile Met Ser Gly Phe Val Ala Gly Ala Cys Ile Ala Gly
115 120 125

Leu Trp Leu Val Ser Tyr Leu Ile Gly Phe Leu Pro Leu Gly Ile Pro
130 135 140

Met Phe Gln Gln Thr Ala Tyr Lys Gly Gln Cys Ser Phe Phe Ala Val

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	145	150	155	160
	Phe His Pro His Phe Val Leu Thr Leu Ser Cys Val Gly Phe Phe Pro			
	165		170	175
5	Ala Met Leu Leu Phe Val Phe Phe Tyr Cys Asp Met Leu Lys Ile Ala			
	180		185	190
	Ser Met His Ser Gln Gln Ile Arg Lys Met Glu His Ala Gly Ala Met			
	195	200		205
	Ala Gly Gly Tyr Arg Ser Pro Arg Thr Pro Ser Asp Phe Lys Ala Leu			
	210	215		220
10	Arg Thr Val Ser Val Leu Ile Gly Ser Phe Ala Leu Ser Trp Thr Pro			
	225	230	235	240
	Phe Leu Ile Thr Gly Ile Val Gln Val Ala Cys Gln Glu Cys His Leu			
	245		250	255
15	Tyr Leu Val Leu Glu Arg Tyr Leu Trp Leu Leu Gly Val Gly Asn Ser			
	260	265		270
	Leu Leu Asn Pro Leu Ile Tyr Ala Tyr Trp Gln Lys Glu Val Arg Leu			
	275	280		285
	Gln Leu Tyr His Met Ala Leu Gly Val Lys Lys Val Leu Thr Ser Phe			
	290	295		300
20	Leu Leu Phe Leu Ser Ala Arg Asn Cys Gly Pro Glu Arg Pro Arg Glu			
	305	310	315	320
	Ser Ser Cys His Ile Val Thr Ile Ser Ser Ser Glu Phe Asp Gly			
	325		330	335

(10) INFORMATION FOR SEQ ID NO:9:

- 25 (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1413 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- 30 (ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

ATGGACACTA CCATGGAAGC TGACCTGGGT GCCACTGGCC ACAGGGCCCCG CACAGAGCTT	60
GATGATGAGG ACTCCTACCC CCAAGGTGGC TGGGACACGG TCTTCCTGGT GGCCCTGCTG	120
CTCCTTGGGC TGCCAGCAA TGGGTTGATG GCGTGGCTGG CGGGCTCCCA GGCCCGGCAT	180
35 GGAGCTGGCA CGCGTCTGGC GCTGCTCCTG CTCAGCCTGG CCCTCTCTGA CTTCTTGTTTC	240

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	CTGGCAGCAG CGGCCTTCCA GATCCTAGAG ATCCGGCATG GGGGACACTG GCCGCTGGGG	300
	ACAGCTGCCT GCCGCTTCTA CTACTTCCTA TGGGGCGTGT CCTACTCCTC CGGCCTCTTC	360
	CTGCTGGCCG CCCTCAGCCT CGACCGCTGC CTGCTGGCGC TGTGCCACA CTGGTACCCCT	420
	GGGCACCGCC CAGTCCGCCT GCCCCTCTGG GTCTGCGCCG GTGTCTGGGT GCTGGCCACA	480
5	CTCTTCAGCG TGCCCTGGCT GGTCTTCCCC GAGGCTGCCG TCTGGTGGTA CGACCTGGTC	540
	ATCTGCCTGG ACTTCTGGGA CAGCGAGGAG CTGTCGCTGA GGATGCTGGA GGTCTGGGG	600
	GGCTTCCTGC CTTTCCTCCT GCTGCTCGTC TGCCACGTGC TCACCCAGGC CACAGCCTGT	660
	CGCACCTGCC ACCGCCAACAA GCAGCCCCGA GCCTGCCGGG GCTTCGCCCG TGTGGCCAGG	720
	ACCATTCTGT CAGCCTATGT GGTCTTGAGG CTGCCCTACC AGCTGGCCA GCTGCTCTAC	780
10	CTGGCCTTCC TGTGGGACGT CTACTCTGGC TACCTGCTCT GGGAGGCCCT GGTCTACTCC	840
	GACTACCTGA TCCTACTCAA CAGCTGCCTC AGCCCCTTCC TCTGCCTCAT GGCCAGTGCC	900
	GACCTCCGGA CCCTGCTGCG CTCCGTGCTC TCGTCCTTCG CGGCAGCTCT CTGCGAGGAG	960
	CGGCCGGGCA GCTTCACGCC CACTGAGCCA CAGACCCAGC TAGATTCTGA GGGTCCAAGT	1020
	CTGCCAGAGC CGATGGCAGA GGCCCAGTCA CAGATGGATC CTGTGGCCA GCCTCAGGTG	1080
15	AACCCCACAC TCCAGCCACG ATCGGATCCC ACAGCTCAGC CACAGCTGAA CCCTACGGCC	1140
	CAGCCACAGT CGGATCCCAC AGCCCAGCCA CAGCTGAACC TCATGGCCA GCCACAGTCA	1200
	GATTCTGTGG CCCAGCCACA GGCAGACACT AACGTCCAGA CCCCTGCACC TGCTGCCAGT	1260
	TCTGTGCCCA GTCCCTGTGA TGAAGCTTCC CCAACCCAT CCTCGCATCC TACCCCAGGG	1320
	GCCCTTGAGG ACCCAGCCAC ACCTCCTGCC TCTGAAGGAG AAAGCCCCAG CAGCACCCCG	1380
20	CCAGAGGCAGG CCCCGGGCGC AGGCCCCACG TGA	1413

(11) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 468 amino acids
- (B) TYPE: amino acid
- 25 (C) STRANDEDNESS:
- (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

30	Met Asp Thr Thr Met Glu Ala Asp Leu Gly Ala Thr Gly His Arg Pro	
	1 5 10 15	

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	Arg Thr Glu Leu Asp Asp Glu Asp Ser Tyr Pro Gln Gly Gly Trp Asp			
	20	25	30	
	Thr Val Phe Leu Val Ala Leu Leu Leu Gly Leu Pro Ala Asn Gly			
	35	40	45	
5	Leu Met Ala Trp Leu Ala Gly Ser Gln Ala Arg His Gly Ala Gly Thr			
	50	55	60	
	Arg Leu Ala Leu Leu Leu Ser Leu Ala Leu Ser Asp Phe Leu Phe			
	65	70	75	80
10	Leu Ala Ala Ala Ala Phe Gln Ile Leu Glu Ile Arg His Gly Gly His			
	85	90	95	
	Trp Pro Leu Gly Thr Ala Ala Cys Arg Phe Tyr Tyr Phe Leu Trp Gly			
	100	105	110	
	Val Ser Tyr Ser Ser Gly Leu Phe Leu Leu Ala Ala Leu Ser Leu Asp			
	115	120	125	
15	Arg Cys Leu Leu Ala Leu Cys Pro His Trp Tyr Pro Gly His Arg Pro			
	130	135	140	
	Val Arg Leu Pro Leu Trp Val Cys Ala Gly Val Trp Val Leu Ala Thr			
	145	150	155	160
20	Leu Phe Ser Val Pro Trp Leu Val Phe Pro Glu Ala Ala Val Trp Trp			
	165	170	175	
	Tyr Asp Leu Val Ile Cys Leu Asp Phe Trp Asp Ser Glu Glu Leu Ser			
	180	185	190	
	Leu Arg Met Leu Glu Val Leu Gly Gly Phe Leu Pro Phe Leu Leu Leu			
	195	200	205	
25	Leu Val Cys His Val Leu Thr Gln Ala Thr Arg Thr Cys His Arg Gln			
	210	215	220	
	Gln Gln Pro Ala Ala Cys Arg Gly Phe Ala Arg Val Ala Arg Thr Ile			
	225	230	235	240
30	Leu Ser Ala Tyr Val Val Leu Arg Leu Pro Tyr Gln Leu Ala Gln Leu			
	245	250	255	
	Leu Tyr Leu Ala Phe Leu Trp Asp Val Tyr Ser Gly Tyr Leu Leu Trp			
	260	265	270	
	Glu Ala Leu Val Tyr Ser Asp Tyr Leu Ile Leu Leu Asn Ser Cys Leu			
	275	280	285	
35	Ser Pro Phe Leu Cys Leu Met Ala Ser Ala Asp Leu Arg Thr Leu Leu			
	290	295	300	
	Arg Ser Val Leu Ser Ser Phe Ala Ala Leu Cys Glu Glu Arg Pro			

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	305	310	315	320
	Gly Ser Phe Thr Pro Thr Glu Pro Gln Thr Gln Leu Asp Ser Gly			
	325	330		335
5	Pro Thr Leu Pro Glu Pro Met Ala Glu Ala Gln Ser Gln Met Asp Pro			
	340	345		350
	Val Ala Gln Pro Gln Val Asn Pro Thr Leu Gln Pro Arg Ser Asp Pro			
	355	360		365
	Thr Ala Gln Pro Gln Leu Asn Pro Thr Ala Gln Pro Gln Ser Asp Pro			
	370	375		380
10	Thr Ala Gln Pro Gln Leu Asn Leu Met Ala Gln Pro Gln Ser Asp Ser			
	385	390	395	400
	Val Ala Gln Pro Gln Ala Asp Thr Asn Val Gln Thr Pro Ala Pro Ala			
	405	410		415
15	Ala Ser Ser Val Pro Ser Pro Cys Asp Glu Ala Ser Pro Thr Pro Ser			
	420	425		430
	Ser His Pro Thr Pro Gly Ala Leu Glu Asp Pro Ala Thr Pro Pro Ala			
	435	440		445
	Ser Glu Gly Glu Ser Pro Ser Ser Thr Pro Pro Glu Ala Ala Pro Gly			
	450	455		460
20	Ala Gly Pro Thr			
	465			

(12) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1248 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

30	ATGTCAGGGA TGGAAAAACT TCAGAATGCT TCCTGGATCT ACCAGCAGAA ACTAGAACAG	60
	CCATTCCAGA AACACCTGAA CAGCACCGAG GAGTATCTGG CCTTCCTCTG CGGACCTCGG	120
	CGCAGCCACT TCTTCCTCCC CGTGTCTGTG GTGTATGTGC CAATTTTGT GGTGGGGGTC	180
	ATTGGCAATG TCCTGGTGTG CCTGGTGATT CTGCAGCACC AGGCTATGAA GACGCCACC	240
	AACTACTACC TCTTCAGCCT GGCGGTCTCT GACCTCCTGG TCCTGCTCCT TGGAAATGCC	300

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CTGGAGGTCT ATGAGATGTG GCGCAACTAC CCTTTCTTGT TCGGGCCCGT GGGCTGCTAC	360
TTCAAGACGG CCCTCTTGA GACCGTGTGC TTCGCCTCCA TCCTCAGCAT CACCACCGTC	420
AGCGTGGAGC GCTACGTGGC CATCCTACAC CCGTTCCGCG CCAAACGTGCA GAGCACCCGG	480
CGCCGGGCC TCAGGATCCT CGGCATCGTC TGGGGCTTCT CCGTGCTCTT CTCCCTGCC	540
5 AACACCAGCA TCCATGGCAT CAAGTTCCAC TACTTCCCCA ATGGGTCCCT GGTCCCAGGT	600
TCGGCCACCT GTACGGTCAT CAAGCCCAGT TGGATCTACA ATTTCATCAT CCAGGTCACC	660
TCCTTCCTAT TCTACCTCCT CCCCATGACT GTCATCAGTG TCCTCTACTA CCTCATGGCA	720
CTCAGACTAA AGAAAGACAA ATCTCTTGAG GCAGATGAAG GGAATGCAAA TATTCAAAGA	780
CCCTGCAGAA AATCAGTCAA CAAGATGCTG TTTGTCTTGG TCTTAGTGT TGCTATCTGT	840
10 TGGGGCCCGT TCCACATTGA CCGACTCTTC TTCAGCTTTG TGGAGGAGTG GAGTGAATCC	900
CTGGCTGCTG TGTTCAACCT CGTCCATGTG GTGTCAGGTG TCTTCTTCTA CCTGAGCTCA	960
GCTGTCAACC CCATTATCTA TAACCTACTG TCTCGCCGCT TCCAGGCAGC ATTCCAGAAT	1020
GTGATCTCTT CTTTCCACAA ACAGTGGCAC TCCCAGCATG ACCCACAGTT GCCACCTGCC	1080
CAGCGGAACA TCTTCCTGAC AGAATGCCAC TTTGTGGAGC TGACCGAAGA TATAGGTCCC	1140
15 CAATTCCCAT GTCAGTCATC CATGCACAAAC TCTCACCTCC CAACAGCCCT CTCTAGTGAA	1200
CAGATGTCAA GAACAAACTA TCAAAGCTTC CACTTTAACCA AACACTGA	1248

(13) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:	
20 (A) LENGTH: 415 amino acids	
(B) TYPE: amino acid	
(C) STRANDEDNESS:	
(D) TOPOLOGY: not relevant	
(ii) MOLECULE TYPE: protein	
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:	
25 Met Ser Gly Met Glu Lys Leu Gln Asn Ala Ser Trp Ile Tyr Gln Gln	
1 5 10 15	
Lys Leu Glu Asp Pro Phe Gln Lys His Leu Asn Ser Thr Glu Glu Tyr	
20 25 30	
30 Leu Ala Phe Leu Cys Gly Pro Arg Arg Ser His Phe Phe Leu Pro Val	
35 40 45	
Ser Val Val Tyr Val Pro Ile Phe Val Val Gly Val Ile Gly Asn Val	

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	50	55	60
	Leu Val Cys Leu Val Ile Leu Gln His Gln Ala Met Lys Thr Pro Thr		
65	65	70	75
5	Asn Tyr Tyr Leu Phe Ser Leu Ala Val Ser Asp Leu Leu Val Leu Leu		
	85	90	95
	Leu Gly Met Pro Leu Glu Val Tyr Glu Met Trp Arg Asn Tyr Pro Phe		
	100	105	110
	Leu Phe Gly Pro Val Gly Cys Tyr Phe Lys Thr Ala Leu Phe Glu Thr		
	115	120	125
10	Val Cys Phe Ala Ser Ile Leu Ser Ile Thr Thr Val Ser Val Glu Arg		
	130	135	140
	Tyr Val Ala Ile Leu His Pro Phe Arg Ala Lys Leu Gln Ser Thr Arg		
	145	150	155
15	Arg Arg Ala Leu Arg Ile Leu Gly Ile Val Trp Gly Phe Ser Val Leu		
	165	170	175
	Phe Ser Leu Pro Asn Thr Ser Ile His Gly Ile Lys Phe His Tyr Phe		
	180	185	190
	Pro Asn Gly Ser Leu Val Pro Gly Ser Ala Thr Cys Thr Val Ile Lys		
	195	200	205
20	Pro Met Trp Ile Tyr Asn Phe Ile Ile Gln Val Thr Ser Phe Leu Phe		
	210	215	220
	Tyr Leu Leu Pro Met Thr Val Ile Ser Val Leu Tyr Tyr Leu Met Ala		
	225	230	235
25	240		
	Leu Arg Leu Lys Lys Asp Lys Ser Leu Glu Ala Asp Glu Gly Asn Ala		
	245	250	255
	Asn Ile Gln Arg Pro Cys Arg Lys Ser Val Asn Lys Met Leu Phe Val		
	260	265	270
	Leu Val Leu Val Phe Ala Ile Cys Trp Ala Pro Phe His Ile Asp Arg		
	275	280	285
30	Leu Phe Phe Ser Phe Val Glu Glu Trp Ser Glu Ser Leu Ala Ala Val		
	290	295	300
	Phe Asn Leu Val His Val Val Ser Gly Val Phe Phe Tyr Leu Ser Ser		
	305	310	315
35	320		
	Ala Val Asn Pro Ile Ile Tyr Asn Leu Leu Ser Arg Arg Phe Gln Ala		
	325	330	335
	Ala Phe Gln Asn Val Ile Ser Ser Phe His Lys Gln Trp His Ser Gln		
	340	345	350

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His	Asp	Pro	Gln	Leu	Pro	Pro	Ala	Gln	Arg	Asn	Ile	Phe	Leu	Thr	Glu
355								360							365

Cys	His	Phe	Val	Glu	Leu	Thr	Glu	Asp	Ile	Gly	Pro	Gln	Phe	Pro	Cys
370							375								380

5	Gln	Ser	Ser	Met	His	Asn	Ser	His	Leu	Pro	Thr	Ala	Leu	Ser	Ser	Glu
385							390					395			400	

Gln	Met	Ser	Arg	Thr	Asn	Tyr	Gln	Ser	Phe	His	Phe	Asn	Lys	Thr
405							410							415

(14) INFORMATION FOR SEQ ID NO:13:

- 10 (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1173 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- 15 (ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

ATGCCAGATA	CTAATAGCAC	AATCAATTAA	TCACTAAGCA	CTCGTGTAC	TTTAGCATT	60	
TTTATGTCCT	TAGTAGCTTT	TGCTATAATG	CTAGGAAATG	CTTGCGTCAT	TTTAGCTTT	120	
GTGGTGGACA	AAAACCTTAG	ACATCGAAGT	AGTTATTTTT	TTCTTAACCT	GGCCATCTCT	180	
20	GACTTCTTG	TGGGTGTGAT	CTCCATTCT	TTGTACATCC	CTCACACGCT	GTTCGAATGG	240
GATTTGGAA	AGGAAATCTG	TGTATTTGG	CTCACTACTG	ACTATCTGTT	ATGTACAGCA	300	
TCTGTATATA	ACATTGTCCT	CATCAGCTAT	GATCGATACC	TGTCAGTCTC	AAATGCTGTG	360	
TCTTATAGAA	CTCAACATAC	TGGGTCTTG	AAGATTGTTA	CTCTGATGGT	GGCCGTTGG	420	
GTGCTGGCCT	TCTTAGTGAA	TGGGCAATG	ATTCTAGTTT	CAGAGTCTTG	GAAGGATGAA	480	
25	GGTAGTGAAT	GTGAACCTGG	ATTTTTTCG	GAATGGTACA	TCCTTGCCAT	CACATCATTC	540
TTGGAATTG	TGATCCCAGT	CATCTTAGTC	GCTTATTCA	ACATGAATAT	TTATTGGAGC	600	
CTGTGGAAGC	GTGATCATCT	CAGTAGGTGC	CAAAGCCATC	CTGGACTGAC	TGCTGTCTCT	660	
TCCAACATCT	GTGGACACTC	ATTCAGAGGT	AGACTATCTT	CAAGGAGATC	TCTTCTGCA	720	
TCGACAGAAG	TTCCTGCATC	CTTCATTCA	GAGAGACAGA	GGAGAAAGAG	TAGTCTCATG	780	
30	TTTCCTCAA	GAACCAAGAT	GAATAGCAAT	ACAATTGCTT	CCAAAATGGG	TTCCTTCTCC	840
CAATCAGATT	CTGTAGCTCT	TCACCAAAGG	GAACATGTTG	AACTGCTTAG	AGCCAGGAGA	900	

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TTAGCCAAGT CACTGGCCAT TCTCTTAGGG GTTTTGCTG TTTGCTGGC TCCATATTCT	960
CTGTCACAA TTGTCCTTTC ATTTTATTCC TCAGCAACAG GTCCTAAATC AGTTTGGTAT	1020
AGAATTGCAT TTTGGCTTCA GTGGTTCAAT TCCTTGTCATC ATCCTCTTT GTATCCATTG	1080
TGTCACAAGC GCTTTCAAAA GGCTTTCTTG AAAATATTTT GTATAAAAAA GCAACCTCTA	1140
5 CCATCACAAAC ACAGTCGGTC AGTATCTTCT TAA	1173

(15) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 390 amino acids
- (B) TYPE: amino acid
- 10 (C) STRANDEDNESS:
- (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

Met Pro Asp Thr Asn Ser Thr Ile Asn Leu Ser Leu Ser Thr Arg Val	
15 1 5 10 15	
Thr Leu Ala Phe Phe Met Ser Leu Val Ala Phe Ala Ile Met Leu Gly	
20 20 25 30	
Asn Ala Leu Val Ile Leu Ala Phe Val Val Asp Lys Asn Leu Arg His	
35 35 40 45	
20 Arg Ser Ser Tyr Phe Phe Leu Asn Leu Ala Ile Ser Asp Phe Phe Val	
50 50 55 60	
Gly Val Ile Ser Ile Pro Leu Tyr Ile Pro His Thr Leu Phe Glu Trp	
65 65 70 75 80	
25 Asp Phe Gly Lys Glu Ile Cys Val Phe Trp Leu Thr Thr Asp Tyr Leu	
85 85 90 95	
Leu Cys Thr Ala Ser Val Tyr Asn Ile Val Leu Ile Ser Tyr Asp Arg	
100 100 105 110	
Tyr Leu Ser Val Ser Asn Ala Val Ser Tyr Arg Thr Gln His Thr Gly	
115 115 120 125	
30 Val Leu Lys Ile Val Thr Leu Met Val Ala Val Trp Val Leu Ala Phe	
130 130 135 140	
Leu Val Asn Gly Pro Met Ile Leu Val Ser Glu Ser Trp Lys Asp Glu	
145 145 150 155 160	
35 Gly Ser Glu Cys Glu Pro Gly Phe Phe Ser Glu Trp Tyr Ile Leu Ala	
165 165 170 175	

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	Ile Thr Ser Phe Leu Glu Phe Val Ile Pro Val Ile Leu Val Ala Tyr			
	180	185	190	
	Phe Asn Met Asn Ile Tyr Trp Ser Leu Trp Lys Arg Asp His Leu Ser			
	195	200	205	
5	Arg Cys Gln Ser His Pro Gly Leu Thr Ala Val Ser Ser Asn Ile Cys			
	210	215	220	
	Gly His Ser Phe Arg Gly Arg Leu Ser Ser Arg Arg Ser Leu Ser Ala			
	225	230	235	240
10	Ser Thr Glu Val Pro Ala Ser Phe His Ser Glu Arg Gln Arg Arg Lys			
	245	250	255	
	Ser Ser Leu Met Phe Ser Ser Arg Thr Lys Met Asn Ser Asn Thr Ile			
	260	265	270	
	Ala Ser Lys Met Gly Ser Phe Ser Gln Ser Asp Ser Val Ala Leu His			
	275	280	285	
15	Gln Arg Glu His Val Glu Leu Leu Arg Ala Arg Arg Leu Ala Lys Ser			
	290	295	300	
	Leu Ala Ile Leu Leu Gly Val Phe Ala Val Cys Trp Ala Pro Tyr Ser			
	305	310	315	320
20	Leu Phe Thr Ile Val Leu Ser Phe Tyr Ser Ser Ala Thr Gly Pro Lys			
	325	330	335	
	Ser Val Trp Tyr Arg Ile Ala Phe Trp Leu Gln Trp Phe Asn Ser Phe			
	340	345	350	
	Val Asn Pro Leu Leu Tyr Pro Leu Cys His Lys Arg Phe Gln Lys Ala			
	355	360	365	
25	Phe Leu Lys Ile Phe Cys Ile Lys Lys Gln Pro Leu Pro Ser Gln His			
	370	375	380	
	Ser Arg Ser Val Ser Ser			
	385	390		

(16) INFORMATION FOR SEQ ID NO:15:

- | | |
|----|--|
| 30 | (i) SEQUENCE CHARACTERISTICS: |
| | (A) LENGTH: 30 base pairs |
| | (B) TYPE: nucleic acid |
| | (C) STRANDEDNESS: single |
| | (D) TOPOLOGY: linear |
| 35 | (ii) MOLECULE TYPE: DNA (genomic) |
| | (iv) ANTI-SENSE: NO |
| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO:15: |

GGAAAGCTTA ACGATCCCCA GGAGCAACAT

30

(17) INFORMATION FOR SEQ ID NO:16:

- 5 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 31 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iv) ANTI-SENSE: YES

10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

CTGGGATCCT ACGAGAGCAT TTTTCACACA G
31

(18) INFORMATION FOR SEQ ID NO:17:

- 15 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1128 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

ATGGCGAACG CGAGCGAGCC GGGTGGCAGC GGCGGCGGCG AGGCAGGCCGC CCTGGGCCTC	60
AAGCTGGCCA CGCTCAGCCT GCTGCTGTGC GTGAGCCTAG CGGGCAACGT GCTGTTCGCG	120
CTGCTGATCG TGCAGGGAGCG CAGCCTGCAC CGCGCCCCGT ACTACCTGCT GCTCGACCTG	180
TGCCTGGCCG ACGGGCTGCG CGCGCTCGCC TGCTCTCCGG CCGTCATGCT GGCGGGCGGG	240
25 CGTGCGGCGG CCGCGGCGGG GGCGCCGCCG GGCGCGCTGG GCTGCAAGCT GCTCGCCTTC	300
CTGGCCGCC TCTTCTGCTT CCACGCCGCC TTCTGCTGC TGGCGTGGG CGTCACCCGC	360
TACCTGGCCA TCGCGCACCA CCGCTTCTAT GCAGAGCGCC TGGCCGGCTG GCCGTGCGCC	420
GCCATGCTGG TGTGCGCCGC CTGGCGCTG GCGCTGGCCG CGGCCTTCCC GCCAGTGCTG	480
GACGGCGGTG GCGACGACGA GGACGCGCCG TGCAGCCCTGG AGCAGCGGCC CGACGGCGCC	540
30 CCCGGCGCCG TGGGCTTCCT GCTGCTGCTG GCCGTGGTGG TGGGCGCCAC GCACCTCGTC	600
TACCTCCGCC TGCTCTTCTT CATCCACGAC CGCCGCAAGA TGCAGCCCGC GCGCCTGGTG	660

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CCCCCGTCA	GCCACGACTG	GACCTTCCAC	GGCCCGGGCG	CCACCGGCCA	GGCGGCCGCC	720	
AACTGGACGG	CGGGCTTCGG	CCGCAGGGCCC	ACGCCGCCCC	CGCTTGTGGG	CATCCGGCCC	780	
GCAGGGCCGG	GCCGCGGCGC	GCGCCGCCTC	CTCGTGCTGG	AAGAATTCAA	GACGGAGAAG	840	
AGGCTGTGCA	AGATGTTCTA	CGCCGTCACG	CTGCTCTTCC	TGCTCCTCTG	GGGGCCCTAC	900	
5	GTCGTGGCCA	GCTACCTGCG	GGTCCTGGTG	CGGCCCGGCG	CCGTCCCCCA	GGCCTACCTG	960
	ACGGCCTCCG	TGTGGCTGAC	CTTCGCGCAG	GCCGGCATCA	ACCCCGTCGT	GTGCTTCCTC	1020
	TTCAACAGGG	AGCTGAGGG	CTGCTTCAGG	GCCCAGTTCC	CCTGCTGCCA	GAGCCCCCGG	1080
	ACCACCCAGG	CGACCCATCC	CTGCGACCTG	AAAGGCATTG	GTTCATGA		1128

(19) INFORMATION FOR SEQ ID NO:18:

- 10 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 375 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: not relevant
- 15 (ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

Met	Ala	Asn	Ala	Ser	Glu	Pro	Gly	Gly	Ser	Gly	Gly	Gly	Glu	Ala	Ala	
1														10	15	
Ala	Leu	Gly	Leu	Lys	Leu	Ala	Thr	Leu	Ser	Leu	Leu	Leu	Cys	Val	Ser	
20														25	30	
Leu	Ala	Gly	Asn	Val	Leu	Phe	Ala	Leu	Leu	Ile	Val	Arg	Glu	Arg	Ser	
35														40	45	
Leu	His	Arg	Ala	Pro	Tyr	Tyr	Leu	Leu	Leu	Asp	Leu	Cys	Leu	Ala	Asp	
50														55	60	
25	Gly	Leu	Arg	Ala	Leu	Ala	Cys	Leu	Pro	Ala	Val	Met	Leu	Ala	Ala	
	65						70					75			80	
Arg	Ala	Ala	Ala	Ala	Ala	Gly	Ala	Pro	Pro	Gly	Ala	Leu	Gly	Cys	Lys	
85														90	95	
30	Leu	Leu	Ala	Phe	Leu	Ala	Ala	Leu	Phe	Cys	Phe	His	Ala	Ala	Phe	Leu
														100	105	
															110	
	Leu	Leu	Gly	Val	Gly	Val	Thr	Arg	Tyr	Leu	Ala	Ile	Ala	His	His	Arg
														115	120	
															125	
	Phe	Tyr	Ala	Glu	Arg	Leu	Ala	Gly	Trp	Pro	Cys	Ala	Ala	Met	Leu	Val
														130	135	
															140	

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	Cys Ala Ala Trp Ala Leu Ala Leu Ala Ala Ala Phe Pro Pro Val Leu	
	145 150 155 160	
	Asp Gly Gly Gly Asp Asp Glu Asp Ala Pro Cys Ala Leu Glu Gln Arg	
	165 170 175	
5	Pro Asp Gly Ala Pro Gly Ala Leu Gly Phe Leu Leu Leu Leu Ala Val	
	180 185 190	
	Val Val Gly Ala Thr His Leu Val Tyr Leu Arg Leu Leu Phe Phe Ile	
	195 200 205	
10	His Asp Arg Arg Lys Met Arg Pro Ala Arg Leu Val Pro Ala Val Ser	
	210 215 220	
	His Asp Trp Thr Phe His Gly Pro Gly Ala Thr Gly Gln Ala Ala Ala	
	225 230 235 240	
	Asn Trp Thr Ala Gly Phe Gly Arg Gly Pro Thr Pro Pro Ala Leu Val	
	245 250 255	
15	Gly Ile Arg Pro Ala Gly Pro Gly Arg Gly Ala Arg Arg Leu Leu Val	
	260 265 270	
	Leu Glu Glu Phe Lys Thr Glu Lys Arg Leu Cys Lys Met Phe Tyr Ala	
	275 280 285	
20	Val Thr Leu Leu Phe Leu Leu Trp Gly Pro Tyr Val Val Ala Ser	
	290 295 300	
	Tyr Leu Arg Val Leu Val Arg Pro Gly Ala Val Pro Gln Ala Tyr Leu	
	305 310 315 320	
	Thr Ala Ser Val Trp Leu Thr Phe Ala Gln Ala Gly Ile Asn Pro Val	
	325 330 335	
25	Val Cys Phe Leu Phe Asn Arg Glu Leu Arg Asp Cys Phe Arg Ala Gln	
	340 345 350	
	Phe Pro Cys Cys Gln Ser Pro Arg Thr Thr Gln Ala Thr His Pro Cys	
	355 360 365	
30	Asp Leu Lys Gly Ile Gly Leu	
	370 375	

(20) INFORMATION FOR SEQ ID NO:19:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1002 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: DNA (genomic)

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

ATGAACACCA	CAGTGATGCA	AGGCTTCAAC	AGATCTGAGC	GGTGCCCCAG	AGACACTCGG	60	
ATAGTACAGC	TGGTATTCCC	AGCCCTCTAC	ACAGTGGTTT	TCTTGACCAG	CATCCTGCTG	120	
AATACTTGG	CTCTGTGGGT	GTTTGTTCAC	ATCCCCAGCT	CCTCCACCTT	CATCATCTAC	180	
5	CTCAAAAACA	CTTTGGTGGC	CGACTTGATA	ATGACACTCA	TGCTTCCTTT	CAAATCCTC	240
	TCTGACTCAC	ACCTGGCACC	CTGGCAGCTC	AGAGCTTTG	TGTGTCGTTT	TTCTTCGGTG	300
	ATATTTATG	AGACCATGTA	TGTGGGCATC	GTGCTGTTAG	GGCTCATAGC	CTTGACAGA	360
	TTCCTCAAGA	TCATCAGACC	TTTGAGAAAT	ATTTTCTAA	AAAAACCTGT	TTTTGCAAAA	420
	ACGGTCTCAA	TCTTCATCTG	GTTCTTTTG	TTCTTCATCT	CCCTGCCAAA	TACGATCTTG	480
10	AGCAACAAGG	AAGCAACACC	ATCGTCTGTG	AAAAAGTGTG	CTTCCTTAAA	GGGGCCTCTG	540
	GGGCTGAAAT	GGCATCAAAT	GGTAAATAAC	ATATGCCAGT	TTATTTCTG	GACTGTTTT	600
	ATCCTAATGC	TTGTGTTTA	TGTGGTTATT	GCAAAAAAAG	TATATGATTC	TTATAGAAAG	660
	TCCAAAAGTA	AGGACAGAAA	AAACAACAAA	AAGCTGGAAG	GCAAAAGTATT	TGTTGTCGTG	720
	GCTGTCTTCT	TTGTGTTTT	TGCTCCATT	CATTTGCCA	GAGTTCCATA	TACTCACAGT	780
15	CAAACCAACA	ATAAGACTGA	CTGTAGACTG	CAAATCAAC	TGTTTATTGC	TAAAGAAACA	840
	ACTCTCTTT	TGGCAGCAAC	TAACATTTGT	ATGGATCCCT	TAATATACAT	ATTCTTATGT	900
	AAAAAATTCA	CAGAAAAGCT	ACCATGTATG	CAAGGGAGAA	AGACCACAGC	ATCAAGCCAA	960
	GAAAATCATA	GCAGTCAGAC	AGACAACATA	ACCTTAGGCT	GA		1002

(21) INFORMATION FOR SEQ ID NO:20:

20 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 333 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: not relevant

25 (ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

Met	Asn	Thr	Thr	Val	Met	Gln	Gly	Phe	Asn	Arg	Ser	Glu	Arg	Cys	Pro	
1					5				10					15		
30	Arg	Asp	Thr	Arg	Ile	Val	Gln	Leu	Val	Phe	Pro	Ala	Leu	Tyr	Thr	Val
					20				25					30		

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	Val Phe Leu Thr Gly Ile Leu Leu Asn Thr Leu Ala Leu Trp Val Phe			
	35	40	45	
	Val His Ile Pro Ser Ser Ser Thr Phe Ile Ile Tyr Leu Lys Asn Thr			
	50	55	60	
5	Leu Val Ala Asp Leu Ile Met Thr Leu Met Leu Pro Phe Lys Ile Leu			
	65	70	75	80
	Ser Asp Ser His Leu Ala Pro Trp Gln Leu Arg Ala Phe Val Cys Arg			
	85	90	95	
10	Phe Ser Ser Val Ile Phe Tyr Glu Thr Met Tyr Val Gly Ile Val Leu			
	100	105	110	
	Leu Gly Leu Ile Ala Phe Asp Arg Phe Leu Lys Ile Ile Arg Pro Leu			
	115	120	125	
	Arg Asn Ile Phe Leu Lys Lys Pro Val Phe Ala Lys Thr Val Ser Ile			
	130	135	140	
15	Phe Ile Trp Phe Phe Leu Phe Ile Ser Leu Pro Asn Thr Ile Leu			
	145	150	155	160
	Ser Asn Lys Glu Ala Thr Pro Ser Ser Val Lys Lys Cys Ala Ser Leu			
	165	170	175	
20	Lys Gly Pro Leu Gly Leu Lys Trp His Gln Met Val Asn Asn Ile Cys			
	180	185	190	
	Gln Phe Ile Phe Trp Thr Val Phe Ile Leu Met Leu Val Phe Tyr Val			
	195	200	205	
	Val Ile Ala Lys Lys Val Tyr Asp Ser Tyr Arg Lys Ser Lys Ser Lys			
	210	215	220	
25	Asp Arg Lys Asn Asn Lys Lys Leu Glu Gly Lys Val Phe Val Val Val			
	225	230	235	240
	Ala Val Phe Phe Val Cys Phe Ala Pro Phe His Phe Ala Arg Val Pro			
	245	250	255	
30	Tyr Thr His Ser Gln Thr Asn Asn Lys Thr Asp Cys Arg Leu Gln Asn			
	260	265	270	
	Gln Leu Phe Ile Ala Lys Glu Thr Thr Leu Phe Leu Ala Ala Thr Asn			
	275	280	285	
	Ile Cys Met Asp Pro Leu Ile Tyr Ile Phe Leu Cys Lys Lys Phe Thr			
	290	295	300	
35	Glu Lys Leu Pro Cys Met Gln Gly Arg Lys Thr Thr Ala Ser Ser Gln			
	305	310	315	320
	Glu Asn His Ser Ser Gln Thr Asp Asn Ile Thr Leu Gly			

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330

(22) INFORMATION FOR SEQ ID NO:21:

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 1122 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

10	ATGGCCAACA CTACCGGAGA GCCTGAGGAG GTGAGCGGCG CTCTGTCCCC ACCGTCCGCA	60
	TCAGCTTATG TGAAGCTGGT ACTGCTGGGA CTGATTATGT GCGTGAGCCT GGCGGGTAAC	120
	GCCATCTTGT CCCTGCTGGT GCTCAAGGAG CGTGCCCTGC ACAAGGCTCC TTACTACTTC	180
	CTGCTGGACC TGTGCCTGGC CGATGGCATA CGCTCTGCCG TCTGCTTCCC CTTTGTGCTG	240
	GCTTCTGTGC GCCACGGCTC TTCATGGACC TTCAGTGCAC TCAGCTGCAA GATTGTGGCC	300
15	TTTATGGCCG TGCTCTTTG CTTCCATGCG GCCTTCATGC TGTTCTGCAT CAGCGTCACC	360
	CGCTACATGG CCATGCCCA CCACCGCTTC TACGCCAAGC GCATGACACT CTGGACATGC	420
	GCGGCTGTCA TCTGCATGGC CTGGACCCCTG TCTGTGGCCA TGGCCTTCCC ACCTGTCTTT	480
	GACGTGGGCA CCTACAAGTT TATTCGGGAG GAGGACCAGT GCATCTTGA GCATCGCTAC	540
	TTCAAGGCCA ATGACACGCT GGGCTTCATG CTTATGTTGG CTGTGCTCAT GGCAGCTACC	600
20	CATGCTGTCT ACGGCAAGCT GCTCCTCTTC GAGTATCGTC ACCGCAAGAT GAAGCCAGTG	660
	CAGATGGTGC CAGCCATCAG CCAGAACTGG ACATTCCATG GTCCCGGGGC CACCGGCCAG	720
	GCTGCTGCCA ACTGGATCGC CGGCTTTGGC CGTGGGCCCA TGCCACCAAC CCTGCTGGGT	780
	ATCCGGCAGA ATGGGCATGC AGCCAGCCGG CGGCTACTGG GCATGGACGA GGTCAAGGGT	840
	GAAAAGCAGC TGGGCCGCAT GTTCTACGGC ATCACACTGC TCTTTCTGCT CCTCTGGTCA	900
25	CCCTACATCG TGGCCTGCTA CTGGCGAGTG TTTGTGAAAG CCTGTGCTGT GCCCCACCGC	960
	TACCTGGCCA CTGCTGTTG GATGAGCTTC GCCCAGGCTG CCGTCAACCC AATTGTCTGC	1020
	TTCCCTGCTCA ACAAGGACCT CAAGAACGTGC CTGACCAACTC ACGCCCCCTG CTGGGGCACA	1080
	GGAGGTGCCCG CGGCTCCAG AGAACCCCTAC TGTGTCATGT GA	1122

(23) INFORMATION FOR SEQ ID NO:22:

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(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 373 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 5 (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

	Met Ala Asn Thr Thr Gly Glu Pro Glu Glu Val Ser Gly Ala Leu Ser	
	1 5 10 15	
10	Pro Pro Ser Ala Ser Ala Tyr Val Lys Leu Val Leu Leu Gly Leu Ile	
	20 25 30	
	Met Cys Val Ser Leu Ala Gly Asn Ala Ile Leu Ser Leu Leu Val Leu	
	35 40 45	
15	Lys Glu Arg Ala Leu His Lys Ala Pro Tyr Tyr Phe Leu Leu Asp Leu	
	50 55 60	
	Cys Leu Ala Asp Gly Ile Arg Ser Ala Val Cys Phe Pro Phe Val Leu	
	65 70 75 80	
	Ala Ser Val Arg His Gly Ser Ser Trp Thr Phe Ser Ala Leu Ser Cys	
	85 90 95	
20	Lys Ile Val Ala Phe Met Ala Val Leu Phe Cys Phe His Ala Ala Phe	
	100 105 110	
	Met Leu Phe Cys Ile Ser Val Thr Arg Tyr Met Ala Ile Ala His His	
	115 120 125	
25	Arg Phe Tyr Ala Lys Arg Met Thr Leu Trp Thr Cys Ala Ala Val Ile	
	130 135 140	
	Cys Met Ala Trp Thr Leu Ser Val Ala Met Ala Phe Pro Pro Val Phe	
	145 150 155 160	
	Asp Val Gly Thr Tyr Lys Phe Ile Arg Glu Glu Asp Gln Cys Ile Phe	
	165 170 175	
30	Glu His Arg Tyr Phe Lys Ala Asn Asp Thr Leu Gly Phe Met Leu Met	
	180 185 190	
	Leu Ala Val Leu Met Ala Ala Thr His Ala Val Tyr Gly Lys Leu Leu	
	195 200 205	
35	Leu Phe Glu Tyr Arg His Arg Lys Met Lys Pro Val Gln Met Val Pro	
	210 215 220	
	Ala Ile Ser Gln Asn Trp Thr Phe His Gly Pro Gly Ala Thr Gly Gln	
	225 230 235 240	

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	Ala Ala Ala Asn Trp Ile Ala Gly Phe Gly Arg Gly Pro Met Pro Pro	
	245	250 255
	Thr Leu Leu Gly Ile Arg Gln Asn Gly His Ala Ala Ser Arg Arg Leu	
	260	265 270
5	Leu Gly Met Asp Glu Val Lys Gly Glu Lys Gln Leu Gly Arg Met Phe	
	275	280 285
	Tyr Ala Ile Thr Leu Leu Phe Leu Leu Trp Ser Pro Tyr Ile Val	
	290	295 300
10	Ala Cys Tyr Trp Arg Val Phe Val Lys Ala Cys Ala Val Pro His Arg	
	305	310 315 320
	Tyr Leu Ala Thr Ala Val Trp Met Ser Phe Ala Gln Ala Ala Val Asn	
	325	330 335
	Pro Ile Val Cys Phe Leu Leu Asn Lys Asp Leu Lys Lys Cys Leu Thr	
	340	345 350
15	Thr His Ala Pro Cys Trp Gly Thr Gly Gly Ala Pro Ala Pro Arg Glu	
	355	360 365
	Pro Tyr Cys Val Met	
	370	

(24) INFORMATION FOR SEQ ID NO:23:

- | | |
|----|-----------------------------------|
| 20 | (i) SEQUENCE CHARACTERISTICS: |
| | (A) LENGTH: 1053 base pairs |
| | (B) TYPE: nucleic acid |
| | (C) STRANDEDNESS: single |
| | (D) TOPOLOGY: linear |
| 25 | (ii) MOLECULE TYPE: DNA (genomic) |

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

	ATGGCTTG AACAGAACCA GTCAACAGAT TATTATTATG AGGAAAATGA AATGAATGGC	60
	ACTTATGACT ACAGTCAATA TGAATTGATC TGTATCAAAG AAGATGTCAG AGAATTGCA	120
	AAAGTTTCC TCCCTGTATT CCTCACAAATA GCTTCTGTCA TTGGACTTGC AGGCAATTCC	180
30	ATGGTAGTGG CAATTTATGC CTATTACAAG AAACAGAGAA CCAAAACAGA TGTGTACATC	240
	CTGAATTGCG TGTAGCAGA TTTACTCCTT CTATTCACTC TGCCTTTTG GGCTGTTAAT	300
	GCAGTTCATG GGTGGGTTTT AGGGAAAATA ATGTGAAAA TAACTTCAGC CTTGTACACA	360
	CTAAACTTTG TCTCTGGAAT GCAGTTCTG GCTTGCATCA GCATAGACAG ATATGTGGCA	420
	GTAACTAATG TCCCCAGCCA ATCAGGAGTG GGAAAACCAT GCTGGATCAT CTGTTCTGT	480

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	GTCTGGATGG CTGCCATCTT GCTGAGCATA CCCCAGCTGG TTTTTTATAAC ACTAAATGAC	540
	AATGCTAGGT GCATTCCCAT TTTCCCCCGC TACCTAGGAA CATCAATGAA AGCATTGATT	600
	CAAATGCTAG AGATCTGCAT TGGATTTGTA GTACCCTTTC TTATTATGGG GGTGTGCTAC	660
	TTTATCACGG CAAGGACACT CATGAAGATG CCAAACATTA AAATATCTCG ACCCCTAAAAA	720
5	GTTCTGCTCA CAGTCGTTAT AGTTTCATT GTCACTCAAC TGCCTTATAA CATTGTCAAG	780
	TTCTGCCGAG CCATAGACAT CATCTACTCC CTGATCACCA GCTGCAACAT GAGCAAACGC	840
	ATGGACATCG CCATCCAAGT CACAGAAAGC ATTGCACTCT TTCACAGCTG CCTCAACCCA	900
	ATCCTTTATG TTTTTATGGG AGCATCTTTC AAAAACTACG TTATGAAAGT GGCCAAGAAA	960
	TATGGGTCCCT GGAGAAAGACA GAGACAAAGT GTGGAGGAGT TTCCTTTGA TTCTGAGGGT	1020
10	CCTACAGAGC CAACCAGTAC TTTAGCATT TAA	1053

(25) INFORMATION FOR SEQ ID NO:24:

- (i) SEQUENCE CHARACTERISTICS:

 - (A) LENGTH: 350 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

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	115	120	125
	Phe Leu Ala Cys Ile Ser Ile Asp Arg Tyr Val Ala Val Thr Asn Val		
	130	135	140
	Pro Ser Gln Ser Gly Val Gly Lys Pro Cys Trp Ile Ile Cys Phe Cys		
5	145	150	155
	Val Trp Met Ala Ala Ile Leu Leu Ser Ile Pro Gln Leu Val Phe Tyr		
	165	170	175
	Thr Val Asn Asp Asn Ala Arg Cys Ile Pro Ile Phe Pro Arg Tyr Leu		
	180	185	190
10	Gly Thr Ser Met Lys Ala Leu Ile Gln Met Leu Glu Ile Cys Ile Gly		
	195	200	205
	Phe Val Val Pro Phe Leu Ile Met Gly Val Cys Tyr Phe Ile Thr Ala		
	210	215	220
15	Arg Thr Leu Met Lys Met Pro Asn Ile Lys Ile Ser Arg Pro Leu Lys		
	225	230	235
	Val Leu Leu Thr Val Val Ile Val Phe Ile Val Thr Gln Leu Pro Tyr		
	245	250	255
	Asn Ile Val Lys Phe Cys Arg Ala Ile Asp Ile Ile Tyr Ser Leu Ile		
	260	265	270
20	Thr Ser Cys Asn Met Ser Lys Arg Met Asp Ile Ala Ile Gln Val Thr		
	275	280	285
	Glu Ser Ile Ala Leu Phe His Ser Cys Leu Asn Pro Ile Leu Tyr Val		
	290	295	300
25	Phe Met Gly Ala Ser Phe Lys Asn Tyr Val Met Lys Val Ala Lys Lys		
	305	310	315
	Tyr Gly Ser Trp Arg Arg Gln Arg Gln Ser Val Glu Glu Phe Pro Phe		
	325	330	335
	Asp Ser Glu Gly Pro Thr Glu Pro Thr Ser Thr Phe Ser Ile		
	340	345	350

30 (26) INFORMATION FOR SEQ ID NO:25:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1116 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

	ATGCCAGGAA ACGCCACCCC AGTGACCACC ACTGCCCCGT GGGCCTCCCT GGGCCTCTCC	60
	GCCAAGACCT GCAACAACGT GTCCTTCGAA GAGAGCAGGA TAGTCCTGGT CGTGGTGTAC	120
	AGCGCGGTGT GCACGCTGGG GGTGCCGGCC AACTGCCTGA CTGCGTGGCT GGCGCTGCTG	180
5	CAGGTACTGC AGGGCAACGT GCTGGCCGTC TACCTGCTCT GCCTGGCACT CTGCGAAGTG	240
	CTGTACACAG GCACGCTGCC ACTCTGGTC ATCTATATCC GCAACCAGCA CCGCTGGACC	300
	CTAGGCCTGC TGGCCTCGAA GGTGACCGCC TACATCTTCT TCTGCAACAT CTACGTCAGC	360
	ATCCTCTTCC TGTGCTGCAT CTCCTGCGAC CGCTTCGTGG CCGTGGTGTAA CGCGCTGGAG	420
	AGTCGGGGCC GCCGCCGCCG GAGGACCGCC ATCCTCATCT CCGCCTGCAT CTTCATCCTC	480
10	GTCGGGATCG TTCACTACCC GGTGTTCCAG ACGGAAGACA AGGAGACCTG CTTTGACATG	540
	CTGCAGATGG ACAGCAGGAT TGCCGGGTAC TACTACGCCA GGTTCACCGT TGGCTTGCC	600
	ATCCCTCTCT CCATCATCGC CTTCACCAAC CACCGGATTT TCAGGAGCAT CAAGCAGAGC	660
	ATGGGCTTAA GCGCTGCCA GAAGGCCAAG GTGAAGCACT CGGCCATCGC GGTGGTTGTC	720
	ATCTTCCTAG TCTGCTTCGC CCCGTACAC CTGGTTCTCC TCGTCAAAGC CGCTGCCTT	780
15	TCCTACTACA GAGGAGACAG GAACGCCATG TGCGGCTTGG AGGAAAGGCT GTACACAGCC	840
	TCTGTGGTGT TTCTGTGCCT GTCCACGGTG AACGGCGTGG CTGACCCCAT TATCTACGTG	900
	CTGGCCACGG ACCATTCCCG CCAAGAACGTG TCCAGAACATCC ATAAGGGGTG GAAAGAGTGG	960
	TCCATGAAGA CAGACGTCAC CAGGCTCACC CACAGCAGGG ACACCGAGGA GCTGCAGTCG	1020
	CCCGTGGCCC TTGCAGACCA CTACACCTTC TCCAGGCCCG TGCAACCCACC AGGGTCACCA	1080
20	TGCCCTGCAA AGAGGCTGAT TGAGGGAGTCC TGCTGA	1116

(28) INFORMATION FOR SEQ ID NO:26:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 371 amino acids
- (B) TYPE: amino acid
- 25 (C) STRANDEDNESS:
- (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

30	Met Pro Gly Asn Ala Thr Pro Val Thr Thr Thr Ala Pro Trp Ala Ser	
	1	5
		10
		15

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	Leu	Gly	Leu	Ser	Ala	Lys	Thr	Cys	Asn	Asn	Val	Ser	Phe	Glu	Glu	Ser
							20				25					30
	Arg	Ile	Val	Leu	Val	Val	Val	Tyr	Ser	Ala	Val	Cys	Thr	Leu	Gly	Val
							35				40					45
5	Pro	Ala	Asn	Cys	Leu	Thr	Ala	Trp	Leu	Ala	Leu	Leu	Gln	Val	Leu	Gln
							50				55					60
	Gly	Asn	Val	Leu	Ala	Val	Tyr	Leu	Leu	Cys	Leu	Ala	Leu	Cys	Glu	Leu
							65				70					80
10	Leu	Tyr	Thr	Gly	Thr	Leu	Pro	Leu	Trp	Val	Ile	Tyr	Ile	Arg	Asn	Gln
							85				90					95
	His	Arg	Trp	Thr	Leu	Gly	Leu	Leu	Ala	Ser	Lys	Val	Thr	Ala	Tyr	Ile
							100				105					110
	Phe	Phe	Cys	Asn	Ile	Tyr	Val	Ser	Ile	Leu	Phe	Leu	Cys	Cys	Ile	Ser
							115				120					125
15	Cys	Asp	Arg	Phe	Val	Ala	Val	Val	Tyr	Ala	Leu	Glu	Ser	Arg	Gly	Arg
							130				135					140
	Arg	Arg	Arg	Arg	Thr	Ala	Ile	Leu	Ile	Ser	Ala	Cys	Ile	Phe	Ile	Leu
							145				150					160
20	Val	Gly	Ile	Val	His	Tyr	Pro	Val	Phe	Gln	Thr	Glu	Asp	Lys	Glu	Thr
							165				170					175
	Cys	Phe	Asp	Met	Leu	Gln	Met	Asp	Ser	Arg	Ile	Ala	Gly	Tyr	Tyr	Tyr
							180				185					190
	Ala	Arg	Phe	Thr	Val	Gly	Phe	Ala	Ile	Pro	Leu	Ser	Ile	Ile	Ala	Phe
							195				200					205
25	Thr	Asn	His	Arg	Ile	Phe	Arg	Ser	Ile	Lys	Gln	Ser	Met	Gly	Leu	Ser
							210				215					220
	Ala	Ala	Gln	Lys	Ala	Lys	Val	Lys	His	Ser	Ala	Ile	Ala	Val	Val	Val
							225				230					240
30	Ile	Phe	Leu	Val	Cys	Phe	Ala	Pro	Tyr	His	Leu	Val	Leu	Leu	Val	Lys
							245				250					255
	Ala	Ala	Ala	Phe	Ser	Tyr	Tyr	Arg	Gly	Asp	Arg	Asn	Ala	Met	Cys	Gly
							260				265					270
	Leu	Glu	Glu	Arg	Leu	Tyr	Thr	Ala	Ser	Val	Val	Phe	Leu	Cys	Leu	Ser
							275				280					285
35	Thr	Val	Asn	Gly	Val	Ala	Asp	Pro	Ile	Ile	Tyr	Val	Leu	Ala	Thr	Asp
							290				295					300

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	His Ser Arg Gln Glu Val Ser Arg Ile His Lys Gly Trp Lys Glu Trp			
	305	310	315	320
	Ser Met Lys Thr Asp Val Thr Arg Leu Thr His Ser Arg Asp Thr Glu			
	325	330	335	
5	Glu Leu Gln Ser Pro Val Ala Leu Ala Asp His Tyr Thr Phe Ser Arg			
	340	345	350	
	Pro Val His Pro Pro Gly Ser Pro Cys Pro Ala Lys Arg Leu Ile Glu			
	355	360	365	
10	Glu Ser Cys			
	370			

(28) INFORMATION FOR SEQ ID NO:27:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1113 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

ATGGCGAACT ATAGCCATGC AGCTGACAAC ATTTTGCAAA ATCTCTCGCC TCTAACAGCC	60
20 TTTCTGAAAC TGACTTCCTT GGGTTTCATA ATAGGAGTCA GCGTGGTGGG CAACCTCCTG	120
ATCTCCATTG TGCTAGTGAA AGATAAGACC TTGCATAGAG CACCTTACTA CTTCCTGTTG	180
GATCTTGCT GTTCAGATAT CCTCAGATCT GCAATTGTT TCCCATTGTG GTTCAACTCT	240
GTCAAAAATG GCTCTACCTG GACTTATGGG ACTCTGACTT GCAAAGTGAT TGCCTTCTG	300
GGGGTTTGTG CCTGTTCCA CACTGTTTC ATGCTTTCT GCATCAGTGT CACCAGATAC	360
25 TTAGCTATCG CCCATCACCG CTTCTATACA AAGAGGCTGA CCTTTGGAC GTGTCTGGCT	420
GTGATCTGTA TGGTGTGGAC TCTGTCTGTG GCCATGGCAT TTCCCCGGT TTTAGACGTG	480
GGCACTTACT CATTCAATTAG GGAGGAAGAT CAATGCACCT TCCAACACCG CTCCTTCAGG	540
GCTAATGATT CCTTAGGATT TATGCTGCTT CTTGCTCTCA TCCTCCTAGC CACACAGCTT	600
GTCTACCTCA AGCTGATATT TTTCGTCCAC GATCGAAGAA AAATGAAGCC AGTCCAGTTT	660
30 GTAGCAGCAG TCAGGCCAGAA CTGGACTTTT CATGGTCCTG GAGCCAGTGG CCAGGCAGCT	720
GCCAATTGGC TAGCAGGATT TGGAAAGGGT CCCACACCAC CCACCTTGCT GGGCATCAGG	780
CAAAATGCAA ACACCACAGG CAGAAGAAGG CTATTGGTCT TAGACGAGTT CAAAATGGAG	840

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AAAAGAATCA	GCAGAATGTT	CTATATAATG	ACTTTCTGT	TTCTAACCTT	GTGGGGCCCC	900
TACCTGGTGG	CCTGTTATTG	GAGAGTTTT	GCAAGAGGGC	CTGTAGTACC	AGGGGGATTT	960
CTAACAGCTG	CTGTCTGGAT	GAGTTTGCC	CAAGCAGGAA	TCAATCCTT	TGTCTGCATT	1020
TTCTCAAACA	GGGAGCTGAG	GCGCTGTTTC	AGCACAAACCC	TTCTTTACTG	CAGAAAATCC	1080
5	AGGTTACCAA	GGGAACCTTA	CTGTGTTATA	TGA		1113

(29) INFORMATION FOR SEQ ID NO:28:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 370 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

15	Met Ala Asn Tyr Ser His Ala Ala Asp Asn Ile Leu Gln Asn Leu Ser	1	5	10	15
	Pro Leu Thr Ala Phe Leu Lys Leu Thr Ser Leu Gly Phe Ile Ile Gly	20	25	30	
	Val Ser Val Val Gly Asn Leu Leu Ile Ser Ile Leu Leu Val Lys Asp	35	40	45	
20	Lys Thr Leu His Arg Ala Pro Tyr Tyr Phe Leu Leu Asp Leu Cys Cys	50	55	60	
	Ser Asp Ile Leu Arg Ser Ala Ile Cys Phe Pro Phe Val Phe Asn Ser	65	70	75	80
25	Val Lys Asn Gly Ser Thr Trp Thr Tyr Gly Thr Leu Thr Cys Lys Val	85	90	95	
	Ile Ala Phe Leu Gly Val Leu Ser Cys Phe His Thr Ala Phe Met Leu	100	105	110	
	Phe Cys Ile Ser Val Thr Arg Tyr Leu Ala Ile Ala His His Arg Phe	115	120	125	
30	Tyr Thr Lys Arg Leu Thr Phe Trp Thr Cys Leu Ala Val Ile Cys Met	130	135	140	
	Val Trp Thr Leu Ser Val Ala Met Ala Phe Pro Pro Val Leu Asp Val	145	150	155	160
	Gly Thr Tyr Ser Phe Ile Arg Glu Glu Asp Gln Cys Thr Phe Gln His				

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	165	170	175
	Arg Ser Phe Arg Ala Asn Asp Ser Leu Gly Phe Met Leu Leu Ala		
	180	185	190
5	Leu Ile Leu Leu Ala Thr Gln Leu Val Tyr Leu Lys Leu Ile Phe Phe		
	195	200	205
	Val His Asp Arg Arg Lys Met Lys Pro Val Gln Phe Val Ala Ala Val		
	210	215	220
10	Ser Gln Asn Trp Thr Phe His Gly Pro Gly Ala Ser Gly Gln Ala Ala		
	225	230	235
	240		
	Ala Asn Trp Leu Ala Gly Phe Gly Arg Gly Pro Thr Pro Pro Thr Leu		
	245	250	255
	Leu Gly Ile Arg Gln Asn Ala Asn Thr Thr Gly Arg Arg Arg Leu Leu		
	260	265	270
15	Val Leu Asp Glu Phe Lys Met Glu Lys Arg Ile Ser Arg Met Phe Tyr		
	275	280	285
	Ile Met Thr Phe Leu Phe Leu Thr Leu Trp Gly Pro Tyr Leu Val Ala		
	290	295	300
	Cys Tyr Trp Arg Val Phe Ala Arg Gly Pro Val Val Pro Gly Gly Phe		
	305	310	315
	320		
20	Leu Thr Ala Ala Val Trp Met Ser Phe Ala Gln Ala Gly Ile Asn Pro		
	325	330	335
	Phe Val Cys Ile Phe Ser Asn Arg Glu Leu Arg Arg Cys Phe Ser Thr		
	340	345	350
25	Thr Leu Leu Tyr Cys Arg Lys Ser Arg Leu Pro Arg Glu Pro Tyr Cys		
	355	360	365
	Val Ile		
	370		

(30) INFORMATION FOR SEQ ID NO:29:

(i) SEQUENCE CHARACTERISTICS:

30 (A) LENGTH: 1080 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

ATGCAGGTCC CGAACAGCAC CGGCCGGAC AACGCGACGC TGCAGATGCT GCGGAACCCG 60

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	GCGATCGCGG	TGGCCCTGCC	CGTGGTGTAC	TCGCTGGTGG	CGGCAGTCAG	CATCCCAGGC	120
	AACCTCTTCT	CTCTGTGGGT	GCTGTGCCGG	CGCATGGGC	CCAGATCCCC	GTCGGTCATC	180
	TTCATGATCA	ACCTGAGCGT	CACGGACCTG	ATGCTGGCCA	GCGTGTGEC	TTTCAAATC	240
	TACTACCATT	GCAACCGCCA	CCACTGGTA	TTCGGGGTGC	TGCTTGCAA	CGTGGTGACC	300
5	GTGGCCTTT	ACGCAAACAT	GTATTCCAGC	ATCCTCACCA	TGACCTGTAT	CAGCGTGGAG	360
	CGCTTCCTGG	GGGTCTGTA	CCCGCTCAGC	TCCAAGCGCT	GGCGCCGCCG	TCGTTACGCG	420
	GTGGCCGCGT	GTGCAGGGAC	CTGGCTGCTG	CTCCTGACCG	CCCTGTGCC	GCTGGCGCGC	480
	ACCGATCTCA	CCTACCCGGT	GCACGCCCTG	GGCATCATCA	CCTGCTTCGA	CGTCCTCAAG	540
	TGGACGATGC	TCCCCAGCGT	GGCCATGTGG	GCCGTGTTCC	TCTTCACCAT	CTTCATCCTG	600
10	CTGTTCTCA	TCCCCTTCGT	GATCACCGTG	GCTTGTACA	CGGCCACCAT	CCTCAAGCTG	660
	TTGCGCACGG	AGGAGGGCGCA	CGGCCGGGAG	CAGCGGAGGC	GCGCGGTGGG	CCTGGCCGCG	720
	GTGGTCTTGC	TGGCCTTGT	CACCTGCTTC	GCCCCAAACA	ACTTCGTGCT	CCTGGCGCAC	780
	ATCGTGAGCC	GCCTGTTCTA	CGGCAAGAGC	TACTACCACG	TGTACAAGCT	CACGCTGTGT	840
	CTCAGCTGCC	TCAACAACTG	TCTGGACCCG	TTTGTATT	ACTTTGCGTC	CCGGGAATT	900
15	CAGCTGCGCC	TGCGGGATA	TTTGGGCTGC	CGCCGGGTGC	CCAGAGACAC	CCTGGACACG	960
	CGCCGCGAGA	GCCTCTTCTC	CGCCAGGACC	ACGTCCGTGC	GCTCCGAGGC	CGGTGCGCAC	1020
	CCTGAAGGGA	TGGAGGGAGC	CACCAGGCC	GGCCTCCAGA	GGCAGGAGAG	TGTGTTCTGA	1080

(31) INFORMATION FOR SEQ ID NO:30:

(i) SEQUENCE CHARACTERISTICS:

20 (A) LENGTH: 359 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: protein

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

Met	Gln	Val	Pro	Asn	Ser	Thr	Gly	Pro	Asp	Asn	Ala	Thr	Leu	Gln	Met	
1															15	
Leu	Arg	Asn	Pro	Ala	Ile	Ala	Val	Ala	Leu	Pro	Val	Val	Tyr	Ser	Leu	
															30	
30	Val	Ala	Ala	Val	Ser	Ile	Pro	Gly	Asn	Leu	Phe	Ser	Leu	Trp	Val	Leu

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	35	40	45
	Cys Arg Arg Met Gly Pro Arg Ser Pro Ser Val Ile Phe Met Ile Asn		
	50	55	60
	Leu Ser Val Thr Asp Leu Met Leu Ala Ser Val Leu Pro Phe Gln Ile		
5	65	70	75
	Tyr Tyr His Cys Asn Arg His His Trp Val Phe Gly Val Leu Leu Cys		
	85	90	95
	Asn Val Val Thr Val Ala Phe Tyr Ala Asn Met Tyr Ser Ser Ile Leu		
	100	105	110
10	Thr Met Thr Cys Ile Ser Val Glu Arg Phe Leu Gly Val Leu Tyr Pro		
	115	120	125
	Leu Ser Ser Lys Arg Trp Arg Arg Arg Tyr Ala Val Ala Ala Cys		
	130	135	140
15	Ala Gly Thr Trp Leu Leu Leu Thr Ala Leu Cys Pro Leu Ala Arg		
	145	150	155
	Thr Asp Leu Thr Tyr Pro Val His Ala Leu Gly Ile Ile Thr Cys Phe		
	165	170	175
	Asp Val Leu Lys Trp Thr Met Leu Pro Ser Val Ala Met Trp Ala Val		
	180	185	190
20	Phe Leu Phe Thr Ile Phe Ile Leu Leu Phe Leu Ile Pro Phe Val Ile		
	195	200	205
	Thr Val Ala Cys Tyr Thr Ala Thr Ile Leu Lys Leu Leu Arg Thr Glu		
	210	215	220
25	Glu Ala His Gly Arg Glu Gln Arg Arg Arg Ala Val Gly Leu Ala Ala		
	225	230	235
	Val Val Leu Leu Ala Phe Val Thr Cys Phe Ala Pro Asn Asn Phe Val		
	245	250	255
	Leu Leu Ala His Ile Val Ser Arg Leu Phe Tyr Gly Lys Ser Tyr Tyr		
	260	265	270
30	His Val Tyr Lys Leu Thr Leu Cys Leu Ser Cys Leu Asn Asn Cys Leu		
	275	280	285
	Asp Pro Phe Val Tyr Tyr Phe Ala Ser Arg Glu Phe Gln Leu Arg Leu		
	290	295	300
35	Arg Glu Tyr Leu Gly Cys Arg Arg Val Pro Arg Asp Thr Leu Asp Thr		
	305	310	315
	Arg Arg Glu Ser Leu Phe Ser Ala Arg Thr Thr Ser Val Arg Ser Glu		
	325	330	335

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Ala Gly Ala His Pro Glu Gly Met Glu Gly Ala Thr Arg Pro Gly Leu
340 345 350

Gln Arg Gln Glu Ser Val Phe
355

5 (32) INFORMATION FOR SEQ ID NO:31:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1503 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

	ATGGAGCGTC CCTGGGAGGA CAGCCCAGGC CGGGAGGGGG CAGCTGAGGG CTCGCCCTGTG	60
	CCAGTCGCCG CGGGGGCGCG CTCCGGTGCC GCGCGAGTG GCACAGGCTG GCAGCCATGG	120
15	GCTGAGTGCC CGGGACCAA GGGGAGGGGG CAACTGCTGG CGACCGCCGG CCCTTGCCT	180
	CGCTGGCCCG CCCCCCTCGCC TGCCAGCTCC AGCCCCGCC CGGGAGCGGC GTCCGCTCAC	240
	TCGGTTCAAG GCAGCGCGAC TGCAGGTGGC GCACGACCAG GGCGCAGACC TTGGGGCGCG	300
	CGGCCCATGG AGTCGGGGCT GCTGCGGCCG GCGCCGGTGA GCGAGGTCAT CGTCCTGCAT	360
	TACAACATACA CGGGCAAGCT CCGCGGTGCG AGCTACCAGC CGGGTGCCGG CCTGCGCGCC	420
20	GACGCCGTGG TGTGCTGGC GGTGTGCGCC TTCATCGTGC TAGAGAATCT AGCCGTGTTG	480
	TTGGTGCTCG GACGCCACCC GCGCTTCCAC GCTCCCATGT TCCTGCTCCT GGGCAGCCTC	540
	ACGTTGTCGG ATCTGCTGGC AGGCGCCGCC TACGCCGCCA ACATCCTACT GTCGGGGCCG	600
	CTCACGCTGA AACTGTCCCC CGCGCTCTGG TTCGCACGGG AGGGAGGCCT TTTCGTGGCA	660
	CTCACTGCGT CCGTGCTGAG CCTCCTGGCC ATCGCGCTGG AGCGCAGCCT CACCATGGCG	720
25	CGCAGGGGGC CGCGCCCGT CTCCAGTCGG GGGCGCACGC TGGCGATGGC AGCCGCGGCC	780
	TGGGGCGTGT CGCTGCTCCT CGGGCTCCTG CCAGCGCTGG GCTGGAATTG CCTGGGTGCG	840
	CTGGACGCTT GCTCCACTGT CTTGCCGCTC TACGCCAAGG CCTACGTGCT CTTCTGCGTG	900
	CTCGCCTTCG TGGGCATCCT GGCGCGATC TGTGCACTCT ACGCGCGCAT CTACTGCCAG	960
	GTACGCGCCA ACGCGCGCG CCTGCCGGCA CGGCCCGGGA CTGCGGGGAC CACCTCGACC	1020
30	CGGGCGCGTC GCAAGCCGCG CTCTCTGGCC TTGCTGCGCA CGCTCAGCGT GGTGCTCCTG	1080

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GCCTTTGTGG	CATGTTGGGG	CCCCCTCTTC	CTGCTGCTGT	TGCTCGACGT	GGCGTGCCCG	1140
GCGCGCACCT	GTCCTGTACT	CCTGCAGGCC	GATCCCTTCC	TGGGACTGGC	CATGGCCAAC	1200
TCACTTCTGA	ACCCCACATCAT	CTACACGCTC	ACCAACCGCG	ACCTGCGCCA	CGCGCTCCTG	1260
CGCCTGGTCT	GCTGCGGACG	CCACTCCTGC	GGCAGAGACC	CGAGTGGCTC	CCAGCAGTCG	1320
5	GCGAGCGCGG	CTGAGGCTTC	CGGGGGCCTG	CGCCGCTGCC	TGCCCCCGGG	1380
	AGCTTCAGCG	GCTCGGAGCG	CTCATCGCCC	CAGCGCGACG	GGCTGGACAC	1440
	ACAGGCAGCC	CCGGTGCACC	CACAGCCGCC	CGGACTCTGG	TATCAGAACCC	1500
	TGA					1503

(33) INFORMATION FOR SEQ ID NO:32:

- 10 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 500 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: not relevant
- 15 (ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

Met	Glu	Arg	Pro	Trp	Glu	Asp	Ser	Pro	Gly	Pro	Glu	Gly	Ala	Ala	Glu	
1				5					10						15	
Gly	Ser	Pro	Val	Pro	Val	Ala	Ala	Gly	Ala	Arg	Ser	Gly	Ala	Ala	Ala	
20			20					25							30	
Ser	Gly	Thr	Gly	Trp	Gln	Pro	Trp	Ala	Glu	Cys	Pro	Gly	Pro	Lys	Gly	
	35				40										45	
Arg	Gly	Gln	Leu	Leu	Ala	Thr	Ala	Gly	Pro	Leu	Arg	Arg	Trp	Pro	Ala	
	50				55						60					
25	Pro	Ser	Pro	Ala	Ser	Ser	Ser	Pro	Ala	Pro	Gly	Ala	Ala	Ser	Ala	His
	65				70					75						80
Ser	Val	Gln	Gly	Ser	Ala	Thr	Ala	Gly	Gly	Ala	Arg	Pro	Gly	Arg	Arg	
		85							90						95	
30	Pro	Trp	Gly	Ala	Arg	Pro	Met	Glu	Ser	Gly	Leu	Leu	Arg	Pro	Ala	Pro
							100			105						110
Val	Ser	Glu	Val	Ile	Val	Leu	His	Tyr	Asn	Tyr	Thr	Gly	Lys	Leu	Arg	
					115			120								125
Gly	Ala	Ser	Tyr	Gln	Pro	Gly	Ala	Gly	Leu	Arg	Ala	Asp	Ala	Val	Val	
				130				135								140

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	Cys Leu Ala Val Cys Ala Phe Ile Val Leu Glu Asn Leu Ala Val Leu			
145	150	155	160	
	Leu Val Leu Gly Arg His Pro Arg Phe His Ala Pro Met Phe Leu Leu			
	165	170	175	
5	Leu Gly Ser Leu Thr Leu Ser Asp Leu Leu Ala Gly Ala Ala Tyr Ala			
	180	185	190	
	Ala Asn Ile Leu Leu Ser Gly Pro Leu Thr Leu Lys Leu Ser Pro Ala			
	195	200	205	
10	Leu Trp Phe Ala Arg Glu Gly Gly Val Phe Val Ala Leu Thr Ala Ser			
	210	215	220	
	Val Leu Ser Leu Leu Ala Ile Ala Leu Glu Arg Ser Leu Thr Met Ala			
	225	230	235	240
	Arg Arg Gly Pro Ala Pro Val Ser Ser Arg Gly Arg Thr Leu Ala Met			
	245	250	255	
15	Ala Ala Ala Ala Trp Gly Val Ser Leu Leu Gly Leu Leu Pro Ala			
	260	265	270	
	Leu Gly Trp Asn Cys Leu Gly Arg Leu Asp Ala Cys Ser Thr Val Leu			
	275	280	285	
20	Pro Leu Tyr Ala Lys Ala Tyr Val Leu Phe Cys Val Leu Ala Phe Val			
	290	295	300	
	Gly Ile Leu Ala Ala Ile Cys Ala Leu Tyr Ala Arg Ile Tyr Cys Gln			
	305	310	315	320
	Val Arg Ala Asn Ala Arg Arg Leu Pro Ala Arg Pro Gly Thr Ala Gly			
	325	330	335	
25	Thr Thr Ser Thr Arg Ala Arg Arg Lys Pro Arg Ser Leu Ala Leu Leu			
	340	345	350	
	Arg Thr Leu Ser Val Val Leu Leu Ala Phe Val Ala Cys Trp Gly Pro			
	355	360	365	
30	Leu Phe Leu Leu Leu Leu Asp Val Ala Cys Pro Ala Arg Thr Cys			
	370	375	380	
	Pro Val Leu Leu Gln Ala Asp Pro Phe Leu Gly Leu Ala Met Ala Asn			
	385	390	395	400
	Ser Leu Leu Asn Pro Ile Ile Tyr Thr Leu Thr Asn Arg Asp Leu Arg			
	405	410	415	
35	His Ala Leu Leu Arg Leu Val Cys Cys Gly Arg His Ser Cys Gly Arg			
	420	425	430	
	Asp Pro Ser Gly Ser Gln Gln Ser Ala Ser Ala Ala Glu Ala Ser Gly			

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435	440	445
Gly Leu Arg Arg Cys Leu Pro Pro Gly Leu Asp Gly Ser Phe Ser Gly		
450	455	460
Ser Glu Arg Ser Ser Pro Gln Arg Asp Gly Leu Asp Thr Ser Gly Ser		
5 465	470	475
Thr Gly Ser Pro Gly Ala Pro Thr Ala Ala Arg Thr Leu Val Ser Glu		
485 490 495		
Pro Ala Ala Asp		
500		

10 (34) INFORMATION FOR SEQ ID NO:33:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1029 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

ATGCAAGCCG TCGACAATCT CACCTCTGCG CCTGGGAACA CCAGTCGTG CACCAGAGAC	60
TACAAAATCA CCCAGGTCTT CTTCCCCTG CTCTACACTG TCCTGTTTT TGTGGACTT	120
20 ATCACAAATG GCCTGGCGAT GAGGATTTC TTTCAAATCC GGAGTAAATC AAACTTTATT	180
ATTTTCTTA AGAACACAGT CATTCTGAT CTTCTCATGA TTCTGACTTT TCCATTCAA	240
ATTCTTAGTG ATGCCAAACT GGGAACAGGA CCACTGAGAA CTTTGTGTG TCAAGTTACC	300
TCCGTATAT TTTATTCAC AATGTATATC AGTATTCAT TCCTGGACT GATAACTATC	360
GATCGCTACC AGAACACCAC CAGGCCATT AAAACATCCA ACCCCAAAAA TCTCTGGGG	420
25 GCTAAGATTG TCTCTGTTGT CATCTGGCA TTCATGTTCT TACTCTCTT GCCTAACATG	480
ATTCTGACCA ACAGGCAGCC GAGAGACAAG AATGTGAAGA AATGCTCTT CCTTAAATCA	540
GAGTTGGTC TAGTCTGGCA TGAAATAGTA ATTACATCT GTCAAGTCAT TTTCTGGATT	600
AATTTCTTAA TTGTTATTGT ATGTTATACA CTCATTACAA AAGAACTGTA CCGGTCATAC	660
GTAAGAACGA GGGGTGAGG TAAAGTCCCC AGGAAAAAGG TGAACGTCAA AGTTTCATT	720
30 ATCATTGCTG TATTCTTAT TTGTTTGTT CCTTCCATT TTGCCGAAT TCCTTACACC	780
CTGAGCCAAA CCCGGGATGT CTTTGACTGC ACTGCTGAAA ATACTCTGTT CTATGTGAAA	840

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GAGAGCACTC	TGTGGTTAAC	TTCCTTAAAT	GCATGCCTGG	ATCCGTTCAT	CTATTTTTTC	900
CTTGCAAGT	CCTTCAGAAA	TTCCTTGATA	AGTATGCTGA	AGTGCCCCAA	TTCTGCAACA	960
TCTCTGTCCC	AGGACAATAG	GAAAAAAGAA	CAGGATGGTG	GTGACCCAAA	TGAAGAGACT	1020
CCAATGTAA						1029

5 (35) INFORMATION FOR SEQ ID NO:34:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 342 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: not relevant
- (ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

Met Gln Ala Val Asp Asn Leu Thr Ser Ala Pro Gly Asn Thr Ser Leu						
1	5	10	15			
15 Cys Thr Arg Asp Tyr Lys Ile Thr Gln Val Leu Phe Pro Leu Leu Tyr	20	25	30			
Thr Val Leu Phe Phe Val Gly Leu Ile Thr Asn Gly Leu Ala Met Arg	35	40	45			
20 Ile Phe Phe Gln Ile Arg Ser Lys Ser Asn Phe Ile Ile Phe Leu Lys	50	55	60			
Asn Thr Val Ile Ser Asp Leu Leu Met Ile Leu Thr Phe Pro Phe Lys	65	70	75	80		
Ile Leu Ser Asp Ala Lys Leu Gly Thr Gly Pro Leu Arg Thr Phe Val	85	90	95			
25 Cys Gln Val Thr Ser Val Ile Phe Tyr Phe Thr Met Tyr Ile Ser Ile	100	105	110			
Ser Phe Leu Gly Leu Ile Thr Ile Asp Arg Tyr Gln Lys Thr Thr Arg	115	120	125			
30 Pro Phe Lys Thr Ser Asn Pro Lys Asn Leu Leu Gly Ala Lys Ile Leu	130	135	140			
Ser Val Val Ile Trp Ala Phe Met Phe Leu Leu Ser Leu Pro Asn Met	145	150	155	160		
Ile Leu Thr Asn Arg Gln Pro Arg Asp Lys Asn Val Lys Lys Cys Ser	165	170	175			
35 Phe Leu Lys Ser Glu Phe Gly Leu Val Trp His Glu Ile Val Asn Tyr						

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	180	185	190
	Ile Cys Gln Val Ile Phe Trp Ile Asn Phe Leu Ile Val Ile Val Cys		
	195	200	205
	Tyr Thr Leu Ile Thr Lys Glu Leu Tyr Arg Ser Tyr Val Arg Thr Arg		
5	210	215	220
	Gly Val Gly Lys Val Pro Arg Lys Lys Val Asn Val Lys Val Phe Ile		
	225	230	235
	Ile Ile Ala Val Phe Phe Ile Cys Phe Val Pro Phe His Phe Ala Arg		
	245	250	255
10	Ile Pro Tyr Thr Leu Ser Gln Thr Arg Asp Val Phe Asp Cys Thr Ala		
	260	265	270
	Glu Asn Thr Leu Phe Tyr Val Lys Glu Ser Thr Leu Trp Leu Thr Ser		
	275	280	285
15	Leu Asn Ala Cys Leu Asp Pro Phe Ile Tyr Phe Phe Leu Cys Lys Ser		
	290	295	300
	Phe Arg Asn Ser Leu Ile Ser Met Leu Lys Cys Pro Asn Ser Ala Thr		
	305	310	315
	Ser Leu Ser Gln Asp Asn Arg Lys Lys Glu Gln Asp Gly Gly Asp Pro		
	325	330	335
20	Asn Glu Glu Thr Pro Met		
	340		

(36) INFORMATION FOR SEQ ID NO:35:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1077 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

30	ATGTCGGTCT GCTACCGTCC CCCAGGGAAC GAGACACTGC TGAGCTGGAA GACTTCGCGG	60
	GCCACAGGCA CAGCCTTCCT GCTGCTGGCG GCGCTGCTGG GGCTGCCTGG CAACGGCTTC	120
	GTGGTGTGGA GCTTGCGGGG CTGGCGGCCT GCACGGGGGC GACCGCTGGC GGCCACGCTT	180
	GTGCTGCACC TGGCGCTGGC CGACGGCGCG GTGCTGCTGC TCACGCCGCT CTTTGTGGCC	240
	TTCCTGACCC GGCAGGCCTG GCCGCTGGC CAGGCAGGGCT GCAAGGGCGT GTACTACGTG	300

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TGCGCGCTCA	GCATGTACGC	CAGCGTGCTG	CTCACCGGCC	TGCTCAGCCT	GCAGCGCTGC	360	
CTCGCAGTCA	CCCGCCCCTT	CCTGGCGCCT	CGGCTGCGCA	GCCC GGCCCT	GGCCCGCCGC	420	
CTGCTGCTGG	CGGTCTGGCT	GGCCGCCCTG	TTGCTCGCCG	TCCC GGCCGC	CGTCTACCAC	480	
CACCTGTGGA	GGGACCGCGT	ATGCCAGCTG	TGCCACCCGT	CGCCGGTCCA	CGCCGCCGCC	540	
5	CACCTGAGCC	TGGAGACTCT	GACCGCTTTC	GTGCTTCCTT	TCGGGCTGAT	GCTCGGCTGC	600
	TACAGCGTGA	CGCTGGCACG	GCTGCGGGGC	GCCC GCTGGG	GCTCCGGCG	GCACGGGGCG	660
	CGGGTGGGCC	GGCTGGTGAG	CGCCATCGTG	CTTGCCTTCG	GCTTGCTCTG	GGCCCCCTAC	720
	CACGCAGTCA	ACCTTCTGCA	GGCGGTGCGA	GCGCTGGCTC	CACCGGAAGG	GGCCTTGGCG	780
	AAGCTGGCG	GAGCCGGCCA	GGCGGCGCGA	GCGGGAACTA	CGGCCTTGGC	CTTCTTCAGT	840
10	TCTAGCGTCA	ACCCGGTGCT	CTACGTCTTC	ACCGCTGGAG	ATCTGCTGCC	CCGGGCAGGT	900
	CCCCGTTTCC	TCACGCGGCT	CTTCGAAGGC	TCTGGGGAGG	CCCGAGGGGG	CGGCCGCTCT	960
	AGGGAAGGGA	CCATGGAGCT	CCGA ACTACC	CCTCAGCTGA	AAGTGGTGGG	GCAGGGCCGC	1020
	GGCAATGGAG	ACCCGGGGGG	TGGGATGGAG	AAGGACGGTC	CGGAATGGGA	CCTTTGA	1077

(37) INFORMATION FOR SEQ ID NO:36:

15 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 358 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: not relevant

20 (ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

Met	Ser	Val	Cys	Tyr	Arg	Pro	Pro	Gly	Asn	Glu	Thr	Leu	Leu	Ser	Trp	
1															15	
Lys	Thr	Ser	Arg	Ala	Thr	Gly	Thr	Ala	Phe	Leu	Leu	Leu	Ala	Ala	Leu	
25															30	
Leu	Gly	Leu	Pro	Gly	Asn	Gly	Phe	Val	Val	Trp	Ser	Leu	Ala	Gly	Trp	
															45	
Arg	Pro	Ala	Arg	Gly	Arg	Pro	Leu	Ala	Ala	Thr	Leu	Val	Leu	His	Leu	
															60	
30	Ala	Leu	Ala	Asp	Gly	Ala	Val	Leu	Leu	Thr	Pro	Leu	Phe	Val	Ala	
															80	
	Phe	Leu	Thr	Arg	Gln	Ala	Trp	Pro	Leu	Gly	Gln	Ala	Gly	Cys	Lys	Ala

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	85	90	95
	Val Tyr Tyr Val Cys Ala Leu Ser Met Tyr Ala Ser Val Leu Leu Thr		
	100	105	110
	Gly Leu Leu Ser Leu Gln Arg Cys Leu Ala Val Thr Arg Pro Phe Leu		
5	115	120	125
	Ala Pro Arg Leu Arg Ser Pro Ala Leu Ala Arg Arg Leu Leu Leu Ala		
	130	135	140
	Val Trp Leu Ala Ala Leu Leu Leu Ala Val Pro Ala Ala Val Tyr Arg		
	145	150	155
10	His Leu Trp Arg Asp Arg Val Cys Gln Leu Cys His Pro Ser Pro Val		
	165	170	175
	His Ala Ala Ala His Leu Ser Leu Glu Thr Leu Thr Ala Phe Val Leu		
	180	185	190
15	Pro Phe Gly Leu Met Leu Gly Cys Tyr Ser Val Thr Leu Ala Arg Leu		
	195	200	205
	Arg Gly Ala Arg Trp Gly Ser Gly Arg His Gly Ala Arg Val Gly Arg		
	210	215	220
	Leu Val Ser Ala Ile Val Leu Ala Phe Gly Leu Leu Trp Ala Pro Tyr		
	225	230	240
20	His Ala Val Asn Leu Leu Gln Ala Val Ala Ala Leu Ala Pro Pro Glu		
	245	250	255
	Gly Ala Leu Ala Lys Leu Gly Gly Ala Gly Gln Ala Ala Arg Ala Gly		
	260	265	270
25	Thr Thr Ala Leu Ala Phe Phe Ser Ser Ser Val Asn Pro Val Leu Tyr		
	275	280	285
	Val Phe Thr Ala Gly Asp Leu Leu Pro Arg Ala Gly Pro Arg Phe Leu		
	290	295	300
	Thr Arg Leu Phe Glu Gly Ser Gly Glu Ala Arg Gly Gly Arg Ser		
	305	310	315
	320		
30	Arg Glu Gly Thr Met Glu Leu Arg Thr Thr Pro Gln Leu Lys Val Val		
	325	330	335
	Gly Gln Gly Arg Gly Asn Gly Asp Pro Gly Gly Met Glu Lys Asp		
	340	345	350
35	Gly Pro Glu Trp Asp Leu		
	355		

(38) INFORMATION FOR SEQ ID NO:37:

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- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1005 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - 5 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

ATGCTGGGGA	TCATGGCATG	GAATGCAACT	TGC AAA ACT	GGCTGGCAGC	AGAGGCTGCC	60
CTGGAAAGT	ACTACCTTTC	CATT TTT TAT	GGGATTGAGT	TCGTTGTGGG	AGTCCTTGGA	120
10 AATACCATTG	TTGTTTACGG	CTACATCTTC	TCTCTGAAGA	ACTGGAACAG	CAGTAATATT	180
TATCTCTTTA	ACCTCTCTGT	CTCTGACTTA	GCT TTT CTGT	GCACCCTCCC	CATGCTGATA	240
AGGAGTTATG	CCAATGGAAA	CTGGATATAT	GGAGACGTGC	TCTGCATAAG	CAACCGATAT	300
GTGCTTCATG	CCAACCTCTA	TACCAGCATT	CTCTTCTCA	CTTTTATCAG	CATAGATCGA	360
TACTTGATAA	TTAAGTATCC	TTTCCGAGAA	CAC TT CTGC	AAAAGAAAGA	GT TT GCTATT	420
15 TTAATCTCCT	TGGCCATTG	GG TTT TAGTA	ACCTTAGAGT	TACTACCCAT	ACTTCCCCTT	480
ATAAAATCCTG	TTATAACTGA	CAATGGCACC	ACCTGTAATG	AT TTT GCAAG	TTCTGGAGAC	540
CCCAACTACA	ACCTCATT T A	CAGCATGTGT	CTAACACTGT	TGGGGTTCT	TATT C CTCTT	600
TTTGTGATGT	GT TTT CTTTA	TTACAAGATT	GCTCTCTTCC	TAAAGCAGAG	GAATAGGCAG	660
GTTGCTACTG	CTCTGCCCT	TGAAAAGCCT	CTCAACTTGG	TCATCATGGC	AGTGGTAATC	720
20 TTCTCTGTGC	TTTTTACACC	CTATCACGTC	ATGCGGAATG	TGAGGATCGC	TTCACGCCTG	780
GGGAGTTGGA	AGCAGTATCA	GTGCACTCAG	GTCGT C ATCA	ACTCCTTTA	CATTGTGACA	840
CGGCCTTGG	CCTTTCTGAA	CAGTGT C ATC	AACCCTGTCT	TCTAT TTT TCT	TTTGGGAGAT	900
CACTTCAGGG	ACATGCTGAT	GAATCAACTG	AGACACA A CT	TCAAATCCCT	TACATCCTTT	960
AGCAGATGGG	CTCATGA A CT	CCTACTTCA	TTCAGAGAAA	AGTGA		1005

25 (39) INFORMATION FOR SEQ ID NO:38:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 334 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - 30 (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: protein

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

	Met Leu Gly Ile Met Ala Trp Asn Ala Thr Cys Lys Asn Trp Leu Ala				
1	5	10	15		
5	Ala Glu Ala Ala Leu Glu Lys Tyr Tyr Leu Ser Ile Phe Tyr Gly Ile	20	25	30	
	Glu Phe Val Val Gly Val Leu Gly Asn Thr Ile Val Val Tyr Gly Tyr	35	40	45	
	Ile Phe Ser Leu Lys Asn Trp Asn Ser Ser Asn Ile Tyr Leu Phe Asn	50	55	60	
10	Leu Ser Val Ser Asp Leu Ala Phe Leu Cys Thr Leu Pro Met Leu Ile	65	70	75	80
	Arg Ser Tyr Ala Asn Gly Asn Trp Ile Tyr Gly Asp Val Leu Cys Ile	85	90	95	
15	Ser Asn Arg Tyr Val Leu His Ala Asn Leu Tyr Thr Ser Ile Leu Phe	100	105	110	
	Leu Thr Phe Ile Ser Ile Asp Arg Tyr Leu Ile Ile Lys Tyr Pro Phe	115	120	125	
	Arg Glu His Leu Leu Gln Lys Lys Glu Phe Ala Ile Leu Ile Ser Leu	130	135	140	
20	Ala Ile Trp Val Leu Val Thr Leu Glu Leu Leu Pro Ile Leu Pro Leu	145	150	155	160
	Ile Asn Pro Val Ile Thr Asp Asn Gly Thr Thr Cys Asn Asp Phe Ala	165	170	175	
25	Ser Ser Gly Asp Pro Asn Tyr Asn Leu Ile Tyr Ser Met Cys Leu Thr	180	185	190	
	Leu Leu Gly Phe Leu Ile Pro Leu Phe Val Met Cys Phe Phe Tyr Tyr	195	200	205	
	Lys Ile Ala Leu Phe Leu Lys Gln Arg Asn Arg Gln Val Ala Thr Ala	210	215	220	
30	Leu Pro Leu Glu Lys Pro Leu Asn Leu Val Ile Met Ala Val Val Ile	225	230	235	240
	Phe Ser Val Leu Phe Thr Pro Tyr His Val Met Arg Asn Val Arg Ile	245	250	255	
35	Ala Ser Arg Leu Gly Ser Trp Lys Gln Tyr Gln Cys Thr Gln Val Val	260	265	270	
	Ile Asn Ser Phe Tyr Ile Val Thr Arg Pro Leu Ala Phe Leu Asn Ser				

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280

285

Val Ile Asn Pro Val Phe Tyr Phe Leu Leu Gly Asp His Phe Arg Asp
 290 295 300

5 Met Leu Met Asn Gln Leu Arg His Asn Phe Lys Ser Leu Thr Ser Phe
 305 310 315 320

Ser Arg Trp Ala His Glu Leu Leu Ser Phe Arg Glu Lys
 325 330

(40) INFORMATION FOR SEQ ID NO:39:

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 1296 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:

ATGCAGGCGC TTAACATTAC CCCGGAGCAG TTCTCTCGGC TGCTGCGGGA CCACAACCTG	60
ACGCGGGAGC AGTCATCGC TCTGTACCGG CTGCGACCAGC TCGTCTACAC CCCAGAGCTG	120
CCGGGACGCG CCAAGCTGGC CCTCGTGCTC ACCGGCGTGC TCATCTTCGC CCTGGCGCTC	180
TTTGGCAATG CTCTGGTGTGTT CTACGTGGTG ACCCGCAGCA AGGCCATGCG CACCGTCACC	240
20 AACATCTTTA TCTGCTCCTT GGCGCTCAGT GACCTGCTCA TCACCTTCTT CTGCATTCCC	300
GTCACCATGC TCCAGAACAT TTCCGACAAC TGGCTGGGG GTGCTTTCAT TTGCAAGATG	360
GTGCCATTG TCCAGTCTAC CGCTGTTGTG ACAGAAATGC TCACTATGAC CTGCATTGCT	420
GTGGAAAGGC ACCAGGGACT TGTGCATCCT TTTAAAATGA AGTGGCAATA CACCAACCGA	480
AGGGCTTTCA CAATGCTAGG TGTGGTCTGG CTGGTGGCAG TCATCGTAGG ATCACCCATG	540
25 TGGCACGTGC AACAACTTGA GATCAAATAT GACTTCCTAT ATGAAAAGGA ACACATCTGC	600
TGCTTAGAAG AGTGGACCAG CCCTGTGCAC CAGAAGATCT ACACCACCTT CATCCTTGTC	660
ATCCTCTTCC TCCTGCCTCT TATGGTGATG CTTATTCTGT ACAGTAAAAT TGGTTATGAA	720
CTTGGATAA AGAAAAGAGT TGGGGATGGT TCAGTGCTTC GAACTATTCA TGGAAAAGAA	780
ATGTCCAAAA TAGCCAGGAA GAAGAACGA GCTGTCATTA TGATGGTGAC AGTGGTGGCT	840
30 CTCTTTGCTG TGTGCTGGGC ACCATTCCAT GTTGTCCATA TGATGATTGA ATACAGTAAT	900
TTTGAAAAGG AATATGATGA TGTACAAATC AAGATGATTT TTGCTATCGT GCAAATTATT	960

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GGATTTCCA	ACTCCATCTG	TAATCCCATT	GTCTATGCAT	TTATGAATGA	AAACTTCAAA	1020
AAAAATGTTT	TGTCTGCAGT	TTGTTATTGC	ATAGTAAATA	AAACCTTCTC	TCCAGCACAA	1080
AGGCATGGAA	ATTCAGGAAT	TACAATGATG	CGGAAGAAAAG	CAAAGTTTC	CCTCAGAGAG	1140
AATCCAGTGG	AGGAAACCAA	AGGAGAAGCA	TTCAGTGATG	GCAACATTGA	AGTCAAATTG	1200
5 TGTGAACAGA	CAGAGGAGAA	GAAAAAGCTC	AAACGACATC	TTGCTCTCTT	TAGGTCTGAA	1260
CTGGCTGAGA	ATTCTCCTTT	AGACAGTGGG	CATTAA			1296

(41) INFORMATION FOR SEQ ID NO:40:

- (i) SEQUENCE CHARACTERISTICS:
10 (A) LENGTH: 431 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 40:

15 Met Gln Ala Leu Asn Ile Thr Pro Glu Gln Phe Ser Arg Leu Leu Arg
 1 5 10 15

 Asp His Asn Leu Thr Arg Glu Gln Phe Ile Ala Leu Tyr Arg Leu Arg
 20 25 30

 20 Pro Leu Val Tyr Thr Pro Glu Leu Pro Gly Arg Ala Lys Leu Ala Leu
 35 40 45

 Val Leu Thr Gly Val Leu Ile Phe Ala Leu Ala Leu Phe Gly Asn Ala
 50 55 60

 Leu Val Phe Tyr Val Val Thr Arg Ser Lys Ala Met Arg Thr Val Thr
 65 70 75 80

 25 Asn Ile Phe Ile Cys Ser Leu Ala Leu Ser Asp Leu Leu Ile Thr Phe
 85 90 95

 Phe Cys Ile Pro Val Thr Met Leu Gln Asn Ile Ser Asp Asn Trp Leu
 100 105 110

 30 Gly Gly Ala Phe Ile Cys Lys Met Val Pro Phe Val Gln Ser Thr Ala
 115 120 125

 Val Val Thr Glu Met Leu Thr Met Thr Cys Ile Ala Val Glu Arg His
 130 135 140

 Gln Gly Leu Val His Pro Phe Lys Met Lys Trp Gln Tyr Thr Asn Arg
 145 150 155 160

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	Arg Ala Phe Thr Met Leu Gly Val Val Trp Leu Val Ala Val Ile Val			
	165	170	175	
	Gly Ser Pro Met Trp His Val Gln Gln Leu Glu Ile Lys Tyr Asp Phe			
	180	185	190	
5	Leu Tyr Glu Lys Glu His Ile Cys Cys Leu Glu Glu Trp Thr Ser Pro			
	195	200	205	
	Val His Gln Lys Ile Tyr Thr Thr Phe Ile Leu Val Ile Leu Phe Leu			
	210	215	220	
10	Leu Pro Leu Met Val Met Leu Ile Leu Tyr Ser Lys Ile Gly Tyr Glu			
	225	230	235	240
	Leu Trp Ile Lys Lys Arg Val Gly Asp Gly Ser Val Leu Arg Thr Ile			
	245	250	255	
	His Gly Lys Glu Met Ser Lys Ile Ala Arg Lys Lys Arg Ala Val			
	260	265	270	
15	Ile Met Met Val Thr Val Val Ala Leu Phe Ala Val Cys Trp Ala Pro			
	275	280	285	
	Phe His Val Val His Met Met Ile Glu Tyr Ser Asn Phe Glu Lys Glu			
	290	295	300	
20	Tyr Asp Asp Val Thr Ile Lys Met Ile Phe Ala Ile Val Gln Ile Ile			
	305	310	315	320
	Gly Phe Ser Asn Ser Ile Cys Asn Pro Ile Val Tyr Ala Phe Met Asn			
	325	330	335	
	Glu Asn Phe Lys Lys Asn Val Leu Ser Ala Val Cys Tyr Cys Ile Val			
	340	345	350	
25	Asn Lys Thr Phe Ser Pro Ala Gln Arg His Gly Asn Ser Gly Ile Thr			
	355	360	365	
	Met Met Arg Lys Lys Ala Lys Phe Ser Leu Arg Glu Asn Pro Val Glu			
	370	375	380	
30	Glu Thr Lys Gly Glu Ala Phe Ser Asp Gly Asn Ile Glu Val Lys Leu			
	385	390	395	400
	Cys Glu Gln Thr Glu Glu Lys Lys Leu Lys Arg His Leu Ala Leu			
	405	410	415	
	Phe Arg Ser Glu Leu Ala Glu Asn Ser Pro Leu Asp Ser Gly His			
	420	425	430	

35 (42) INFORMATION FOR SEQ ID NO:41:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 24 base pairs

- 50 -

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:41:

CTGTGTACAG CAGTCGCAG AGTG

24

(43) INFORMATION FOR SEQ ID NO:42:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 24 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:42:

15 GAGTGCCAGG CAGAGCAGGT AGAC

24

(44) INFORMATION FOR SEQ ID NO:43:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 31 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:43:

25 CCCGAATTCC TGCTTGCTCC CAGCTTGGCC C

31

(45) INFORMATION FOR SEQ ID NO:44:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 32 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iv) ANTI-SENSE: YES

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:44:

TGTGGATCCT GCTGTCAAAG GTCCCATTCG GG

32

(46) INFORMATION FOR SEQ ID NO:45:

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

10 (iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:45:

TCACAATGCT AGGTGTGGTC

20

(47) INFORMATION FOR SEQ ID NO:46:

(i) SEQUENCE CHARACTERISTICS:

- 15 (A) LENGTH: 22 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

20 (iv) ANTI-SENSE: YES

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:46:

TGCATAGACA ATGGGATTAC AG

22

(48) INFORMATION FOR SEQ ID NO:47:

(i) SEQUENCE CHARACTERISTICS:

- 25 (A) LENGTH: 511 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:47:

TCACAATGCT AGGTGTGGTC TGGCTGGTGG CAGTCATCGT AGGATCACCC ATGTGGCACG

60

TGCAACAACT TGAGATCAAATATGACTTCC TATATGAAAAA GGAACACATC TGCTGCTTAG

120

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AAGAGTGGAC CAGCCCTGTG CACCAGAAGA TCTACACCAC CTTCATCCTT GTCATCCTCT	180
TCCTCCTGCC TCTTATGGTG ATGCTTATTG TGTACGTAAA ATTGGTTATG AACTTTGGAT	240
AAAGAAAAGA GTTGGGGATG GTTCAGTGCT TCGAACTATT CATGGAAAAG AAATGTCCAA	300
AATAGCCAGG AAGAAGAAC GAGCTGTCAT TATGATGGTG ACAGTGGTGG CTCTCTTGCG	360
5 TGTGTGCTGG GCACCATTCC ATGTTGTCCA TATGATGATT GAATACAGTA ATTTTGAAAAA	420
GGAATATGAT GATGTCACAA TCAAGATGAT TTTTGCTATC GTGCAAATTA TTGGATTTTC	480
CAAECTCCATC TGTAATCCC TTGTCTATGC A	511

(49) INFORMATION FOR SEQ ID NO:48:

- (i) SEQUENCE CHARACTERISTICS:
 - 10 (A) LENGTH: 21 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- 15 (iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:48:

CTGCTTAGAA GAGTGGACCA G	21
-------------------------	----

(50) INFORMATION FOR SEQ ID NO:49:

- (i) SEQUENCE CHARACTERISTICS:
 - 20 (A) LENGTH: 22 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- 25 (iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:49:

CTGTGCACCA GAAGATCTAC AC	22
--------------------------	----

(51) INFORMATION FOR SEQ ID NO:50:

- (i) SEQUENCE CHARACTERISTICS:
 - 30 (A) LENGTH: 21 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

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(ii) MOLECULE TYPE: DNA (genomic)

(iv) ANTI-SENSE: YES

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:50:

CAAGGATGAA GGTGGTGTAG A

21

5 (52) INFORMATION FOR SEQ ID NO:51:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

10

(ii) MOLECULE TYPE: DNA (genomic)

(iv) ANTI-SENSE: YES

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:51:

GTGTAGATCT TCTGGTGCAC AGG

23

15 (53) INFORMATION FOR SEQ ID NO:52:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

20

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:52:

GCAATGCAGG TCATAGTGAG C

21

(54) INFORMATION FOR SEQ ID NO:53:

25

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 27 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

30

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: YES

(iv) ANTI-SENSE: YES

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:53:

TGGAGCATGG TGACGGGAAT GCAGAAG

27

(55) INFORMATION FOR SEQ ID NO:54:

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 27 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

10 (iv) ANTI-SENSE: YES

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:54:

GTGATGAGCA GGTCACTGAG CGCCAAG

27

(56) INFORMATION FOR SEQ ID NO:55:

(i) SEQUENCE CHARACTERISTICS:

- 15 (A) LENGTH: 23 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

20 (iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:55:

GCAATGCAGG CGCTTAACAT TAC

23

(57) INFORMATION FOR SEQ ID NO:56:

(i) SEQUENCE CHARACTERISTICS:

- 25 (A) LENGTH: 22 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

30 (iv) ANTI-SENSE: YES

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:56:

TTGGGTTACA ATCTGAAGGG CA

22

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(58) INFORMATION FOR SEQ ID NO:57:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 23 base pairs
(B) TYPE: nucleic acid
5 (C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:57:

10 ACTCCGTGTC CAGCAGGACT CTG

23

(58) INFORMATION FOR SEQ ID NO:58:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 24 base pairs
(B) TYPE: nucleic acid
15 (C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iv) ANTI-SENSE: YES

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:58:

20 TGC GTGTTCC TGGAC CCTCA CGTG

24

(58) INFORMATION FOR SEQ ID NO:59:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 29 base pairs
(B) TYPE: nucleic acid
25 (C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:59:

30 CAGGCC TTGG ATTTAATGT CAGGGATGG

29

(61) INFORMATION FOR SEQ ID NO:60:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 27 base pairs

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- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

5 (iv) ANTI-SENSE: YES

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:60:

GGAGAGTCAG CTCTGAAAGA ATTCAAGG

27

(62) INFORMATION FOR SEQ ID NO:61:

- 10 (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 27 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

15 (iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:61:

TGATGTGATG CCAGATACTA ATAGCAC

27

(63) INFORMATION FOR SEQ ID NO:62:

- 20 (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 27 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

25 (iv) ANTI-SENSE: YES

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:62:

CCTGATTCCAT TTAGGTGAGA TTGAGAC

27

(64) INFORMATION FOR SEQ ID NO:63:

- 30 (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 26 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

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(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:63:

CCCAAGCTTC CCCAGGTGTA TTTGAT

26

(3) INFORMATION FOR SEQ ID NO:63:

- 5 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 26 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

10 (ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:64:

GTTGGATCCA CATAATGCAT TTTCTC

26

(66) INFORMATION FOR SEQ ID NO:65:

- 15 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1080 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:65:

ATGATTCTCA ACTCTTCTAC TGAAGATGGT ATTAAAAGAA TCCAAGATGA TTGTCCAAA	60
GCTGGAAGGC ATAATTACAT ATTTGTCATG ATTCCTACTT TATACAGTAT CATCTTTGTG	120
GTGGGAATAT TTGGAACACAG CTTGGTGGTG ATAGTCATTT ACTTTTATAT GAAGCTGAAG	180
ACTGTGGCCA GTGTTTTCT TTTGAATTAA GCACTGGCTG ACTTATGCTT TTTACTGACT	240
25 TTGCCACTAT GGGCTGTCTA CACAGCTATG GAATACCGCT GGCCCTTGG CAATTACCTA	300
TGTAAGATTG CTTCAGCCAG CGTCAGTTTC AACCTGTACG CTAGTGTGTT TCTACTCACG	360
TGTCTCAGCA TTGATCGATA CCTGGCTATT GTTCACCCAA TGAAGTCCCG CCTTCGACGC	420
ACAATGCTTG TAGCCAAAGT CACCTGCATC ATCATTGGC TGCTGGCAGG CTTGGCCAGT	480
TTGCCAGCTA TAATCCATCG AAATGTATT TTCATTGAGA ACACCAATAT TACAGTTGT	540
30 GCTTCCATT ATGAGTCCCA AAATTCAACC CTTCCGATAG GGCTGGGCCT GACCAAAAT	600

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ATACTGGGTT	TCCTGTTCC	TTTCTGATC	ATTCTTACAA	GTTATACTCT	TATTTGGAAG	660	
GCCCTAAAGA	AGGCTTATGA	AATTCAGAAG	AACAAACCAA	GAAATGATGA	TATTTTTAAG	720	
ATAATTATGG	CAATTGTGCT	TTTCTTTTC	TTTCCTGGA	TTCCCCACCA	AATATTCACT	780	
TTTCTGGATG	TATTGATTCA	ACTAGGCATC	ATACGTGACT	GTAGAATTGC	AGATATTGTG	840	
5	GACACGGCCA	TGCCTATCAC	CATTTGTATA	GCTTATTTTA	ACAATTGCCT	GAATCCTCTT	900
	TTTTATGGCT	TTCTGGGGAA	AAAATTTAAA	AGATATTTTC	TCCAGCTTCT	AAAATATATT	960
	CCCCCAAAAG	CCAAATCCCA	CTCAAACCTT	TCAACAAAAA	TGAGCACGCT	TTCCCTACCGC	1020
	CCCTCAGATA	ATGTAAGCTC	ATCCACCAAG	AAGCCTGCAC	CATGTTTGA	GGTTGAGTG	1080

(67) INFORMATION FOR SEQ ID NO:66:

- 10 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 359 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: not relevant
- 15 (ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:66:

Met Ile Leu Asn Ser Ser Thr Glu Asp Gly Ile Lys Arg Ile Gln Asp						
1	5	10	15			
Asp Cys Pro Lys Ala Gly Arg His Asn Tyr Ile Phe Val Met Ile Pro						
20	25	30				
Thr Leu Tyr Ser Ile Ile Phe Val Val Gly Ile Phe Gly Asn Ser Leu						
35	40	45				
Val Val Ile Val Ile Tyr Phe Tyr Met Lys Leu Lys Thr Val Ala Ser						
50	55	60				
25	Val Phe Leu Leu Asn Leu Ala Leu Asp Leu Cys Phe Leu Leu Thr					
65	70	75	80			
Leu Pro Leu Trp Ala Val Tyr Thr Ala Met Glu Tyr Arg Trp Pro Phe						
85	90	95				
30	Gly Asn Tyr Leu Cys Lys Ile Ala Ser Ala Ser Val Ser Phe Asn Leu					
100	105	110				
Tyr Ala Ser Val Phe Leu Leu Thr Cys Leu Ser Ile Asp Arg Tyr Leu						
115	120	125				
Ala Ile Val His Pro Met Lys Ser Arg Leu Arg Arg Thr Met Leu Val						

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	130	135	140
	Ala Lys Val Thr Cys Ile Ile Trp Leu Leu Ala Gly Leu Ala Ser		
145	150	155	160
5	Leu Pro Ala Ile Ile His Arg Asn Val Phe Phe Ile Glu Asn Thr Asn		
	165	170	175
	Ile Thr Val Cys Ala Phe His Tyr Glu Ser Gln Asn Ser Thr Leu Pro		
	180	185	190
	Ile Gly Leu Gly Leu Thr Lys Asn Ile Leu Gly Phe Leu Phe Pro Phe		
	195	200	205
10	Leu Ile Ile Leu Thr Ser Tyr Thr Leu Ile Trp Lys Ala Leu Lys Lys		
	210	215	220
	Ala Tyr Glu Ile Gln Lys Asn Lys Pro Arg Asn Asp Asp Ile Phe Lys		
	225	230	235
	240		
15	Ile Ile Met Ala Ile Val Leu Phe Phe Phe Ser Trp Ile Pro His		
	245	250	255
	Gln Ile Phe Thr Phe Leu Asp Val Leu Ile Gln Leu Gly Ile Ile Arg		
	260	265	270
	Asp Cys Arg Ile Ala Asp Ile Val Asp Thr Ala Met Pro Ile Thr Ile		
	275	280	285
20	Cys Ile Ala Tyr Phe Asn Asn Cys Leu Asn Pro Leu Phe Tyr Gly Phe		
	290	295	300
	Leu Gly Lys Phe Lys Arg Tyr Phe Leu Gln Leu Leu Lys Tyr Ile		
	305	310	315
	320		
25	Pro Pro Lys Ala Lys Ser His Ser Asn Leu Ser Thr Lys Met Ser Thr		
	325	330	335
	Leu Ser Tyr Arg Pro Ser Asp Asn Val Ser Ser Ser Thr Lys Lys Pro		
	340	345	350
	Ala Pro Cys Phe Glu Val Glu		
	355		

30 (68) INFORMATION FOR SEQ ID NO:67:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 27 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

35 (ii) MOLECULE TYPE: DNA (genomic)

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:67:

ACCATGGGCA GCCCCTGGAA CGGCAGC

27

(69) INFORMATION FOR SEQ ID NO:68:

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 39 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:68:

AGAACACCACCA CCAGCAGGAC GCGGACGGTC TGCCGGTGG

39

(70) INFORMATION FOR SEQ ID NO:69:

(i) SEQUENCE CHARACTERISTICS:

- 15 (A) LENGTH: 39 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:69:

20 GTCCGCGTCC TGCTGGTGGT GGTTCTGGCA TTTATAATT

39

(71) INFORMATION FOR SEQ ID NO:70:

(i) SEQUENCE CHARACTERISTICS:

- 25 (A) LENGTH: 33 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:70:

CCTGGATCCT TATCCCACCG TCTTCACGTT AGC

33

30 (72) INFORMATION FOR SEQ ID NO:71:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single

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(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:71:

5 CTGGAATTCT CCTGCCAGCA TGGTGA
26

(73) INFORMATION FOR SEQ ID NO:72:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iv) ANTI-SENSE: YES

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:72:

GCAGGATCCT ATATTGCGTG CTCTGTCCCC
30

(74) INFORMATION FOR SEQ ID NO:73:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 999 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:73:

ATGGTGAAC	CCACCCACCG	TGGGATGCAC	ACTTCTCTGC	ACCTCTGGAA	CCGCAGCAGT	60
TACAGACTGC	ACAGCAATGC	CAGTGAGTCC	CTTGGAAAAG	GCTACTCTGA	TGGAGGGTGC	120
TACGAGCAAC	TTTTGTCTC	TCCTGAGGTG	TTTGTGACTC	TGGGTGTCAT	CAGCTTGTG	180
GAGAATATCT	TAGTGATTGT	GGCAATAGCC	AAGAACAAAGA	ATCTGCATTC	ACCCATGTAC	240
30 TTTTCATCT	GCAGCTTGGC	TGTGGCTGAT	ATGCTGGTGA	GCGTTTCAA	TGGATCAGAA	300
ACCATTATCA	TCACCCTATT	AAACAGTACA	GATA CGGATG	CACAGAGTTT	CACAGTGAAT	360
ATTGATAATG	TCATTGACTC	GGTGATCTGT	AGCTCCTTGC	TTGCATCCAT	TTGCAGCCTG	420

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CTTTCAATTG CAGTGGACAG GTACTTTACT ATCTTCTATG CTCTCCAGTA CCATAACATT	480
ATGACAGTTA AGCGGGTTGG GATCAGCATA AGTTGTATCT GGGCAGCTTG CACGGTTCA	540
GGCATTGT TCATCATTAA CTCAGATAGT AGTGCTGTCA TCATCTGCCT CATCACCATG	600
TTCTTCACCA TGCTGGCTCT CATGGCTTCT CTCTATGTCC ACATGTTCCCT GATGGCCAGG	660
5 CTTCACATTA AGAGGATTGC TGCCTCCCC GGCACGGTG CCATCCGCCA AGGTGCCAAT	720
ATGAAGGGAG CGATTACCTT GACCATCCTG ATTGGCGTCT TTGTTGTCTG CTGGGCCCA	780
TTCTTCCTCC ACTTAATATT CTACATCTCT TGTCCCTCAGA ATCCATATTG TGTGTGCTTC	840
ATGTCTCACT TAACTTGTA TCTCATACTG ATCATGTGTA ATTCAATCAT CGATCCTCTG	900
ATTATGCAC TCCGGAGTCA AGAACTGAGG AAAACCTTCA AAGAGATCAT CTGTTGCTAT	960
10 CCCCTGGGAG GCCTTTGTGA CTTGTCTAGC AGATATTAA	999

(75) INFORMATION FOR SEQ ID NO:74:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 332 amino acids
 - (B) TYPE: amino acid
 - 15 (C) STRANDEDNESS:
 - (D) TOPOLOGY: not relevant
- (ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:74:

Met Val Asn Ser Thr His Arg Gly Met His Thr Ser Leu His Leu Trp	
20 1 5 10 15	
Asn Arg Ser Ser Tyr Arg Leu His Ser Asn Ala Ser Glu Ser Leu Gly	
20 25 30	
Lys Gly Tyr Ser Asp Gly Gly Cys Tyr Glu Gln Leu Phe Val Ser Pro	
35 40 45	
25 Glu Val Phe Val Thr Leu Gly Val Ile Ser Leu Leu Glu Asn Ile Leu	
50 55 60	
Val Ile Val Ala Ile Ala Lys Asn Lys Asn Leu His Ser Pro Met Tyr	
65 70 75 80	
30 Phe Phe Ile Cys Ser Leu Ala Val Ala Asp Met Leu Val Ser Val Ser	
85 90 95	
Asn Gly Ser Glu Thr Ile Ile Thr Leu Leu Asn Ser Thr Asp Thr	
100 105 110	
Asp Ala Gln Ser Phe Thr Val Asn Ile Asp Asn Val Ile Asp Ser Val	

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	115	120	125
	Ile Cys Ser Ser Leu Leu Ala Ser Ile Cys Ser Leu Leu Ser Ile Ala		
	130	135	140
5	Val Asp Arg Tyr Phe Thr Ile Phe Tyr Ala Leu Gln Tyr His Asn Ile		
	145	150	155
	Met Thr Val Lys Arg Val Gly Ile Ser Ile Ser Cys Ile Trp Ala Ala		
	165	170	175
10	Cys Thr Val Ser Gly Ile Leu Phe Ile Ile Tyr Ser Asp Ser Ser Ala		
	180	185	190
	Val Ile Ile Cys Leu Ile Thr Met Phe Phe Thr Met Leu Ala Leu Met		
	195	200	205
	Ala Ser Leu Tyr Val His Met Phe Leu Met Ala Arg Leu His Ile Lys		
	210	215	220
15	Arg Ile Ala Val Leu Pro Gly Thr Gly Ala Ile Arg Gln Gly Ala Asn		
	225	230	235
	Met Lys Gly Ala Ile Thr Leu Thr Ile Leu Ile Gly Val Phe Val Val		
	245	250	255
	Cys Trp Ala Pro Phe Phe Leu His Leu Ile Phe Tyr Ile Ser Cys Pro		
	260	265	270
20	Gln Asn Pro Tyr Cys Val Cys Phe Met Ser His Phe Asn Leu Tyr Leu		
	275	280	285
	Ile Leu Ile Met Cys Asn Ser Ile Ile Asp Pro Leu Ile Tyr Ala Leu		
	290	295	300
25	Arg Ser Gln Glu Leu Arg Lys Thr Phe Lys Glu Ile Ile Cys Cys Tyr		
	305	310	315
	Pro Leu Gly Gly Leu Cys Asp Leu Ser Ser Arg Tyr		
	325	330	

(76) INFORMATION FOR SEQ ID NO:75:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 32 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:75:

CCGAAGCTTC GAGCTGAGTA AGGCAGCGGG CT

32

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(77) INFORMATION FOR SEQ ID NO:76:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 31 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

5

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:76:

GTGGAATTCA TTTGCCCTGC CTCAACCCCC A

31

10 (78) INFORMATION FOR SEQ ID NO:77:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1344 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

15

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:77:

ATGGAGCTGC TAAAGCTGAA CCGGAGCGTG CAGGGAACCG GACCCGGGCC GGGGGCTTCC

60

CTGTGCCGCC CGGGGGCGCC TCTCCTCAAC AGCAGCAGTG TGGGCAACCT CAGCTGCGAG

120

20 CCCCTCGCA TTCGCGGAGC CGGGACACGA GAATTGGAGC TGGCCATTAG AATCACTCTT

180

TACGCAGTGA TCTTCCTGAT GAGCGTTGGA GGAAATATGC TCATCATCGT GGTCTGGGA

240

CTGAGCCGCC GCCTGAGGAC TGTCACCAAT GCCTTCCTCC TCTCACTGGC AGTCAGCGAC

300

CTCCTGCTGG CTGTGGCTTG CATGCCCTTC ACCCTCCTGC CCAATCTCAT GGGCACATTG

360

ATCTTGCGCA CCGTCATCTG CAAGGCGGTT TCCTACCTCA TGGGGGTGTC TGTGAGTGTG

420

25 TCCACGCTAA GCCTCGTGGC CATCGCACTG GAGCGATATA GCGCCATCTG CCGACCACTG

480

CAGGCACGAG TGTGGCAGAC GCGCTCCAC GCGGCTCGCG TGATTGTAGC CACGTGGCTG

540

CTGTCCGGAC TACTCATGGT GCCCTACCCC GTGTACACTG TCGTGCAACC AGTGGGGCCT

600

CGTGTGCTGC AGTGCCTGCA TCGCTGGCCC AGTGCCTGGG TCCGCCAGAC CTGGTCCGTA

660

CTGCTGCTTC TGCTCTTGTGTT CTTCATCCA GGTGTGGTTA TGGCCGTGGC CTACGGGCTT

720

30 ATCTCTCGCG AGCTCTACTT AGGGCTTCGC TTTGACGGCG ACAGTGACAG CGACAGCCAA

780

AGCAGGGTCC GAAACCAAGG CGGGCTGCCA GGGGCTGTTC ACCAGAACGG GCGTTGCCGG

840

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CCTGAGACTG	GCGCGGTTGG	CAAAGACAGC	GATGGCTGCT	ACGTGCAACT	TCCACGTTCC	900	
CGGCCTGCC	TGGAGCTGAC	GGCGCTGACG	GCTCCTGGC	CGGGATCCGG	CTCCCGGCC	960	
ACCCAGGCCA	AGCTGCTGGC	TAAGAACGCG	GTGGTGCAGA	TGTTGCTGGT	GATCGTTGTG	1020	
CTTTTTTTTC	TGTGTTGGTT	GCCAGTTTAT	AGTGCCAACA	CGTGGCGCGC	CTTGATGGC	1080	
5	CGGGGTGCAC	ACCGAGCACT	CTCGGGTGCT	CCTATCTCCT	TCATTCACTT	GCTGAGCTAC	1140
	GCCTCGGCCT	GTGTCAACCC	CCTGGTCTAC	TGCTTCATGC	ACCGTCGCTT	TCGCCAGGCC	1200
	TGCCTGGAAA	CTTGCCTCG	CTGCTGCC	CGGCCTCCAC	GAGCTGCC	CAGGGCTCTT	1260
	CCCGATGAGG	ACCCTCCCAC	TCCCTCCATT	GCTTCGCTGT	CCAGGCTTAG	CTACACCACC	1320
	ATCAGCACAC	TGGGCCCTGG	CTGA				1344

10 (79) INFORMATION FOR SEQ ID NO:78:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 447 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:78:

Met	Glu	Leu	Leu	Lys	Leu	Asn	Arg	Ser	Val	Gln	Gly	Thr	Gly	Pro	Gly
1					5				10				15		
20	Pro	Gly	Ala	Ser	Leu	Cys	Arg	Pro	Gly	Ala	Pro	Leu	Leu	Asn	Ser
					20				25				30		
	Ser	Val	Gly	Asn	Leu	Ser	Cys	Glu	Pro	Pro	Arg	Ile	Arg	Gly	Ala
					35			40				45			
25	Thr	Arg	Glu	Leu	Glu	Leu	Ala	Ile	Arg	Ile	Thr	Leu	Tyr	Ala	Val
					50			55				60			
	Phe	Leu	Met	Ser	Val	Gly	Gly	Asn	Met	Leu	Ile	Ile	Val	Val	Leu
					65			70			75				80
	Leu	Ser	Arg	Arg	Leu	Arg	Thr	Val	Thr	Asn	Ala	Phe	Leu	Leu	Ser
					85			90				95			
30	Ala	Val	Ser	Asp	Leu	Leu	Ala	Val	Ala	Cys	Met	Pro	Phe	Thr	Leu
					100			105				110			
	Leu	Pro	Asn	Leu	Met	Gly	Thr	Phe	Ile	Phe	Gly	Thr	Val	Ile	Cys
					115			120				125			

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Ala Val Ser Tyr Leu Met Gly Val Ser Val Ser Val Ser Thr Leu Ser
130 135 140

Leu Val Ala Ile Ala Leu Glu Arg Tyr Ser Ala Ile Cys Arg Pro Leu
145 150 155 160

5 Gln Ala Arg Val Trp Gln Thr Arg Ser His Ala Ala Arg Val Ile Val
165 170 175

Ala Thr Trp Leu Leu Ser Gly Leu Leu Met Val Pro Tyr Pro Val Tyr
180 185 190

Thr Val Val Gln Pro Val Gly Pro Arg Val Leu Gln Cys Val His Arg
10 195 200 205

Trp Pro Ser Ala Arg Val Arg Gln Thr Trp Ser Val Leu Leu Leu Leu
210 215 220

Leu Leu Phe Phe Ile Pro Gly Val Val Met Ala Val Ala Tyr Gly Leu
225 230 235 240

Ile Ser Arg Glu Leu Tyr Leu Gly Leu Arg Phe Asp Gly Asp Ser Asp
15 245 250 255

Ser Asp Ser Gln Ser Arg Val Arg Asn Gln Gly Gly Leu Pro Gly Ala
260 265 270

Val His Gln Asn Gly Arg Cys Arg Pro Glu Thr Gly Ala Val Gly Lys
20 275 280 285

Asp Ser Asp Gly Cys Tyr Val Gln Leu Pro Arg Ser Arg Pro Ala Leu
290 295 300

Glu Leu Thr Ala Leu Thr Ala Pro Gly Pro Gly Ser Gly Ser Arg Pro
305 310 315 320

25 Thr Gln Ala Lys Leu Leu Ala Lys Lys Arg Val Val Arg Met Leu Leu
325 330 335

Val Ile Val Val Leu Phe Phe Leu Cys Trp Leu Pro Val Tyr Ser Ala
340 345 350

Asn Thr Trp Arg Ala Phe Asp Gly Pro Gly Ala His Arg Ala Leu Ser
30 355 360 365

Val Ala Pro Ile Ser Phe Ile His Leu Leu Ser Tyr Ala Ser Ala Cys
370 375 380

Val Asn Pro Leu Val Tyr Cys Phe Met His Arg Arg Phe Arg Gln Ala
385 390 395 400

Cys Leu Glu Thr Cys Ala Arg Cys Cys Pro Arg Pro Pro Arg Ala Arg
35 405 410 415

Pro Arg Ala Leu Pro Asp Glu Asp Pro Pro Thr Pro Ser Ile Ala Ser

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420

425

430

Leu Ser Arg Leu Ser Tyr Thr Thr Ile Ser Thr Leu Gly Pro Gly
 435 440 445

(80) INFORMATION FOR SEQ ID NO:79:

- 5 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 30 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

10 (ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:79:

TGCAAGCTTA AAAAGGAAAA AATGAACAGC

30

(81) INFORMATION FOR SEQ ID NO:80:

- 15 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 30 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:80:

TAAGGATCCC TTCCCTTCAA AACATCCTTG

30

(82) INFORMATION FOR SEQ ID NO:81:

- 25 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1014 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:81:

30	ATGAACAGCA CATGTATTGA AGAACAGCAT GACCTGGATC ACTATTTGTT TCCCATTGTT	60
	TACATCTTG TGATTATACT CAGCATTCCA GCCAATATTG GATCTCTGTG TGTGTCTTTC	120
	CTGCAACCCA AGAAGGAAAG TGAACCTAGGA ATTTACCTCT TCAGTTGTC ACTATCAGAT	180
	TTACTCTATG CATTAACCTCT CCCTTTATGG ATTGATTATA CTTGGAATAA AGACAACCTGG	240

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	ACTTTCTCTC CTGCCTTGTG CAAAGGGAGT GCTTTCTCA TGTACATGAA GTTTTACAGC	300
	AGCACAGCAT TCCTCACCTG CATTGCCGTT GATCGGTATT TGGCTGTTGT CTACCCTTG	360
	AAGTTTTTT TCCTAAGGAC AAGAAGAATT GCACTCATGG TCAGCCTGTC CATCTGGATA	420
	TTGGAAACCA TCTTCAATGC TGTCATGTTG TGGGAAGATG AAACAGTTGT TGAATATTGC	480
5	GATGCCGAAA AGTCTAATT TACTTTATGC TATGACAAAT ACCCTTTAGA GAAATGGCAA	540
	ATCAAACCTCA ACTTGTTCAG GACGTGTACA GGCTATGCAA TACCTTTGGT CACCATCCTG	600
	ATCTGTAACC GGAAAGTCTA CCAAGCTGTG CGGCACAATA AAGCCACGGA AAACAAGGAA	660
	AAGAAGAGAA TCATAAAACT ACTTGTCAAGC ATCACAGTTA CTTTTGTCTT ATGCTTTACT	720
	CCCTTTCATG TGATGTTGCT GATTCGCTGC ATTTTAGAGC ATGCTGTGAA CTTCGAAGAC	780
10	CACAGCAATT CTGGGAAGCG AACTTACACA ATGTATAGAA TCACGGTTGC ATTAACAAGT	840
	TTAAATTGTG TTGCTGATCC AATTCTGTAC TGTTTTGTTA CCGAAACAGG AAGATATGAT	900
	ATGTGGAATA TATTAAAATT CTGCACTGGG AGGTGTAATA CATCACAAAG ACAAAAGAAAA	960
	CGCATACTTT CTGTGTCTAC AAAAGATACT ATGGAATTAG AGGTCCCTGAA GTAG	1014

(83) INFORMATION FOR SEQ ID NO:82:

- 15 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 337 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: not relevant

20 (ii) MOLECULE TYPE: protein

20 (ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:82:

	Met	Asn	Ser	Thr	Cys	Ile	Glu	Glu	Gln	His	Asp	Leu	Asp	His	Tyr	Leu
	1					5				10				15		
	Phe	Pro	Ile	Val	Tyr	Ile	Phe	Val	Ile	Ile	Val	Ser	Ile	Pro	Ala	Asn
25							20			25				30		
	Ile	Gly	Ser	Leu	Cys	Val	Ser	Phe	Leu	Gln	Pro	Lys	Lys	Glu	Ser	Glu
						35			40			45				
	Leu	Gly	Ile	Tyr	Leu	Phe	Ser	Leu	Ser	Leu	Ser	Asp	Leu	Leu	Tyr	Ala
						50			55			60				
30	Leu	Thr	Leu	Pro	Leu	Trp	Ile	Asp	Tyr	Thr	Trp	Asn	Lys	Asp	Asn	Trp
						65			70			75			80	
	Thr	Phe	Ser	Pro	Ala	Leu	Cys	Lys	Gly	Ser	Ala	Phe	Leu	Met	Tyr	Met

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	85	90	95	
	Lys Phe Tyr Ser Ser Thr Ala Phe Leu Thr Cys Ile Ala Val Asp Arg			
	100	105	110	
5	Tyr Leu Ala Val Val Tyr Pro Leu Lys Phe Phe Phe Leu Arg Thr Arg			
	115	120	125	
	Arg Ile Ala Leu Met Val Ser Leu Ser Ile Trp Ile Leu Glu Thr Ile			
	130	135	140	
	Phe Asn Ala Val Met Leu Trp Glu Asp Glu Thr Val Val Glu Tyr Cys			
	145	150	155	160
10	Asp Ala Glu Lys Ser Asn Phe Thr Leu Cys Tyr Asp Lys Tyr Pro Leu			
	165	170	175	
	Glu Lys Trp Gln Ile Asn Leu Asn Leu Phe Arg Thr Cys Thr Gly Tyr			
	180	185	190	
15	Ala Ile Pro Leu Val Thr Ile Leu Ile Cys Asn Arg Lys Val Tyr Gln			
	195	200	205	
	Ala Val Arg His Asn Lys Ala Thr Glu Asn Lys Glu Lys Lys Arg Ile			
	210	215	220	
	Ile Lys Leu Leu Val Ser Ile Thr Val Thr Phe Val Leu Cys Phe Thr			
	225	230	235	240
20	Pro Phe His Val Met Leu Leu Ile Arg Cys Ile Leu Glu His Ala Val			
	245	250	255	
	Asn Phe Glu Asp His Ser Asn Ser Gly Lys Arg Thr Tyr Thr Met Tyr			
	260	265	270	
25	Arg Ile Thr Val Ala Leu Thr Ser Leu Asn Cys Val Ala Asp Pro Ile			
	275	280	285	
	Leu Tyr Cys Phe Val Thr Glu Thr Gly Arg Tyr Asp Met Trp Asn Ile			
	290	295	300	
	Leu Lys Phe Cys Thr Gly Arg Cys Asn Thr Ser Gln Arg Gln Arg Lys			
	305	310	315	320
30	Arg Ile Leu Ser Val Ser Thr Lys Asp Thr Met Glu Leu Glu Val Leu			
	325	330	335	
	Glu			

(84) INFORMATION FOR SEQ ID NO:83:

- 35 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 40 base pairs
 (B) TYPE: nucleic acid

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- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:83:

5 CAGGAAGAAG AAACGAGCTG TCATTATGAT GGTGACAGTG
40

(85) INFORMATION FOR SEQ ID NO:84:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 40 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:84:

15 CACTGTCACC ATCATAATGA CAGCTCGTTT CTTCTTCCTG
40

(86) INFORMATION FOR SEQ ID NO:85:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 30 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:85:

25 GGCCACCGGC AGACCAAACG CGTCCTGCTG
30

(87) INFORMATION FOR SEQ ID NO:86:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 31 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:86:

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CTCCTTCGGT CCTCCTATCG TTGTCAGAAG T
31

(88) INFORMATION FOR SEQ ID NO:87:

- 5 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 37 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:87:

GGAAAAGAAG AGAATCAAAA AACTACTTGT CAGCATC

37

(89) INFORMATION FOR SEQ ID NO:88:

- 15 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 31 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:88:

20 CTCCTTCGGT CCTCCTATCG TTGTCAGAAG T

31

(90) INFORMATION FOR SEQ ID NO:89:

- 25 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1080 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:89:

ATGATTCTCA ACTCTTCTAC TGAAGATGGT ATTAAAAGAA TCCAAGATGA TTGTCCAAA 60

30 GCTGGAAGGC ATAATTACAT ATTTGTCATG ATTCCCTACTT TATACAGTAT CATCTTTGTG 120

GTGGGAATAT TTGGAACAG CTTGGTGGTG ATAGTCATTT ACTTTTATAT GAAGCTGAAG 180

ACTGTGGCCA GTGTTTTCT TTTGAATTAA GCACTGGCTG ACTTATGCTT TTTACTGACT 240

TTGCCACTAT GGGCTGTCTA CACAGCTATG GAATACCGCT GGCCCTTTGG CAATTACCTA 300

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TGTAAGATTG	CTTCAGCCAG	CGTCAGTTTC	AACCTGTACG	CTAGTGTGTT	TCTACTCACG	360	
TGTCTCAGCA	TTGATCGATA	CCTGGCTATT	GTTCACCCAA	TGAAGTCCCG	CCTTCGACGC	420	
ACAATGCTTG	TAGCCAAAGT	CACCTGCATC	ATCATTGGC	TGCTGGCAGG	CTTGGCCAGT	480	
TTGCCAGCTA	TAATCCATCG	AAATGTATTT	TTCATTGAGA	ACACCAATAT	TACAGTTTGT	540	
5	GCTTTCCATT	ATGAGTCCCA	AAATTCAACC	CTTCCGATAG	GGCTGGGCCT	GACCAAAAAT	600
	ATACTGGGTT	TCCTGTTCC	TTTCTGATC	ATTCTTACAA	GTTATACTCT	TATTTGGAAAG	660
	GCCCTAAAGA	AGGCTTATGA	AATTCAAG	AACAAACCAA	GAAATGATGA	TATTAAAAAG	720
	ATAATTATGG	CAATTGTGCT	TTTCTTTTC	TTTCCTGGA	TTCCCCACCA	AATATTCACT	780
	TTTCTGGATG	TATTGATTCA	ACTAGGCATC	ATACGTGACT	GTAGAATTGC	AGATATTGTG	840
10	GACACGGCCA	TGCCTATCAC	CATTTGTATA	GCTTATTTA	ACAATTGCCT	GAATCCTCTT	900
	TTTTATGGCT	TTCTGGGAA	AAAATTTAAA	AGATATTTTC	TCCAGCTTCT	AAAATATATT	960
	CCCCAAAAG	CCAAATCCCA	CTCAAACCTT	TCAACAAAAA	TGAGCACGCT	TTCCCTACCGC	1020
	CCCTCAGATA	ATGTAAGCTC	ATCCACCAAG	AAGCCTGCAC	CATGTTTGA	GGTTGAGTGA	1080

(91) INFORMATION FOR SEQ ID NO:90:

- 15 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 359 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: not relevant
- 20 (ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:90:

Met	Ile	Leu	Asn	Ser	Ser	Thr	Glu	Asp	Gly	Ile	Lys	Arg	Ile	Gln	Asp	
1										5			10		15	
Asp	Cys	Pro	Lys	Ala	Gly	Arg	His	Asn	Tyr	Ile	Phe	Val	Met	Ile	Pro	
25									20		25		30			
Thr	Leu	Tyr	Ser	Ile	Ile	Phe	Val	Val	Gly	Ile	Phe	Gly	Asn	Ser	Leu	
									35		40		45			
Val	Val	Ile	Val	Ile	Tyr	Phe	Tyr	Met	Lys	Leu	Lys	Thr	Val	Ala	Ser	
									50		55		60			
30	Val	Phe	Leu	Leu	Asn	Leu	Ala	Leu	Asp	Leu	Cys	Phe	Leu	Leu	Thr	
									65		70		75		80	
	Leu	Pro	Leu	Trp	Ala	Val	Tyr	Thr	Ala	Met	Glu	Tyr	Arg	Trp	Pro	Phe

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	85	90	95
	Gly Asn Tyr Leu Cys Lys Ile Ala Ser Ala Ser Val Ser Phe Asn Leu		
	100	105	110
5	Tyr Ala Ser Val Phe Leu Leu Thr Cys Leu Ser Ile Asp Arg Tyr Leu		
	115	120	125
	Ala Ile Val His Pro Met Lys Ser Arg Leu Arg Arg Thr Met Leu Val		
	130	135	140
	Ala Lys Val Thr Cys Ile Ile Trp Leu Leu Ala Gly Leu Ala Ser		
	145	150	155
10	Leu Pro Ala Ile Ile His Arg Asn Val Phe Phe Ile Glu Asn Thr Asn		
	165	170	175
	Ile Thr Val Cys Ala Phe His Tyr Glu Ser Gln Asn Ser Thr Leu Pro		
	180	185	190
15	Ile Gly Leu Gly Leu Thr Lys Asn Ile Leu Gly Phe Leu Phe Pro Phe		
	195	200	205
	Leu Ile Ile Leu Thr Ser Tyr Thr Leu Ile Trp Lys Ala Leu Lys Lys		
	210	215	220
	Ala Tyr Glu Ile Gln Lys Asn Lys Pro Arg Asn Asp Asp Ile Lys Lys		
	225	230	235
20	Ile Ile Met Ala Ile Val Leu Phe Phe Phe Ser Trp Ile Pro His		
	245	250	255
	Gln Ile Phe Thr Phe Leu Asp Val Leu Ile Gln Leu Gly Ile Ile Arg		
	260	265	270
25	Asp Cys Arg Ile Ala Asp Ile Val Asp Thr Ala Met Pro Ile Thr Ile		
	275	280	285
	Cys Ile Ala Tyr Phe Asn Asn Cys Leu Asn Pro Leu Phe Tyr Gly Phe		
	290	295	300
	Leu Gly Lys Phe Lys Arg Tyr Phe Leu Gln Leu Leu Lys Tyr Ile		
	305	310	315
30	Pro Pro Lys Ala Lys Ser His Ser Asn Leu Ser Thr Lys Met Ser Thr		
	325	330	335
	Leu Ser Tyr Arg Pro Ser Asp Asn Val Ser Ser Ser Thr Lys Lys Pro		
	340	345	350
35	Ala Pro Cys Phe Glu Val Glu		
	355		

(92) INFORMATION FOR SEQ ID NO:91:

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- (i) SEQUENCE CHARACTERISTICS:

 - (A) LENGTH: 35 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

5

- (ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:91:

CCAAGAAATG ATGATATTAA AAAGATAATT ATGGC

35

(93) INFORMATION FOR SEQ ID NO:92:

10 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 31 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

15 (ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 92:

CTCCTTCGGT CCTCCTATCG TTGTCAGAAG T

31

(94) INFORMATION FOR SEQ ID NO:93:

20 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1080 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 93:

ATGATTCTCA ACTCTTCTAC TGAAGATGGT ATTAAAAAGAA TCCAAGATGA TTGTCCCCAA

60

GCTGGAAAGGC ATAATTACAT ATTTGTCA TG ATTCCCTACTT TATAACAGTAT CATTTTG TG

120

GTGGGAATAT TTGGAAACAG CTTGGTGGTG ATAGTCATTT ACTTTTATAT GAAGCTGAAG

180

ACTGTGGCCA GTGTTTCT TTTGAATTTA GCACGGCTG ACTTATGCTT TTTACTGACTT

240

TTGCCACTAT GGGCTGTCTA CACAGCTATG GAATAACCGCT GGCCCTTTGG CAATTACCTA

300

TGTAAGATTG CTTCAGCCAG CGTCAGTTTC GCCCTGTACG CTAGTGTGTT TCTACTCACGG

360

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ACAATGCTTG TAGCCAAAGT CACCTGCATC ATCATTTGGC TGCTGGCAGG CTTGGCCAGT	480
TTGCCAGCTA TAATCCATCG AAATGTATTTC TTCATTGAGA ACACCAATAT TACAGTTGT	540
GCTTTCCATT ATGAGTCCA AAATTCAACC CTTCCGATAG GGCTGGGCCT GACCAAAAAT	600
ATACTGGGTT TCCTGTTCC TTTCTGATC ATTCTTACAA GTTATACTCT TATTTGGAAG	660
5 GCCCTAAAGA AGGCTTATGA AATTCAAG AACAAACCAA GAAATGATGA TATTTTTAAG	720
ATAATTATGG CAATTGTGCT TTTCTTTTC TTTCTCTGGA TTCCCCACCA AATATTCACT	780
TTTCTGGATG TATTGATTCA ACTAGGCATC ATACGTGACT GTAGAATTGC AGATATTGTG	840
GACACGGCCA TGCCTATCAC CATTGTATA GCTTATTTA ACAATTGCCT GAATCCTCTT	900
TTTTATGGCT TTCTGGGAA AAAATTAAA AGATATTTTC TCCAGCTTCT AAAATATATT	960
10 CCCCAAAAG CCAAATCCA CTAAACCTT TCAACAAAAA TGAGCACGCT TTCCCTACCGC	1020
CCCTCAGATA ATGTAAGCTC ATCCACCAAG AAGCCTGCAC CATGTTTGA GGTTGAGTGA	1080

(95) INFORMATION FOR SEQ ID NO:94:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 359 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: not relevant
- (ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:94:

20	Met Ile Leu Asn Ser Ser Thr Glu Asp Gly Ile Lys Arg Ile Gln Asp			
	1	5	10	15
	Asp Cys Pro Lys Ala Gly Arg His Asn Tyr Ile Phe Val Met Ile Pro			
	20	25	30	
25	Thr Leu Tyr Ser Ile Ile Phe Val Val Gly Ile Phe Gly Asn Ser Leu			
	35	40	45	
	Val Val Ile Val Ile Tyr Phe Tyr Met Lys Leu Lys Thr Val Ala Ser			
	50	55	60	
	Val Phe Leu Leu Asn Leu Ala Leu Ala Asp Leu Cys Phe Leu Leu Thr			
	65	70	75	80
30	Leu Pro Leu Trp Ala Val Tyr Thr Ala Met Glu Tyr Arg Trp Pro Phe			
	85	90	95	
	Gly Asn Tyr Leu Cys Lys Ile Ala Ser Ala Ser Val Ser Phe Ala Leu			

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	100	105	110
	Tyr Ala Ser Val Phe Leu Leu Thr Cys Leu Ser Ile Asp Arg Tyr Leu		
	115	120	125
5	Ala Ile Val His Pro Met Lys Ser Arg Leu Arg Arg Thr Met Leu Val		
	130	135	140
	Ala Lys Val Thr Cys Ile Ile Trp Leu Leu Ala Gly Leu Ala Ser		
	145	150	155
	Leu Pro Ala Ile Ile His Arg Asn Val Phe Phe Ile Glu Asn Thr Asn		
	165	170	175
10	Ile Thr Val Cys Ala Phe His Tyr Glu Ser Gln Asn Ser Thr Leu Pro		
	180	185	190
	Ile Gly Leu Gly Leu Thr Lys Asn Ile Leu Gly Phe Leu Phe Pro Phe		
	195	200	205
15	Leu Ile Ile Leu Thr Ser Tyr Thr Leu Ile Trp Lys Ala Leu Lys Lys		
	210	215	220
	Ala Tyr Glu Ile Gln Lys Asn Lys Pro Arg Asn Asp Asp Ile Phe Lys		
	225	230	235
	Ile Ile Met Ala Ile Val Leu Phe Phe Phe Ser Trp Ile Pro His		
	245	250	255
20	Gln Ile Phe Thr Phe Leu Asp Val Leu Ile Gln Leu Gly Ile Ile Arg		
	260	265	270
	Asp Cys Arg Ile Ala Asp Ile Val Asp Thr Ala Met Pro Ile Thr Ile		
	275	280	285
25	Cys Ile Ala Tyr Phe Asn Asn Cys Leu Asn Pro Leu Phe Tyr Gly Phe		
	290	295	300
	Leu Gly Lys Lys Phe Lys Arg Tyr Phe Leu Gln Leu Leu Lys Tyr Ile		
	305	310	315
	Pro Pro Lys Ala Lys Ser His Ser Asn Leu Ser Thr Lys Met Ser Thr		
	325	330	335
30	Leu Ser Tyr Arg Pro Ser Asp Asn Val Ser Ser Ser Thr Lys Lys Pro		
	340	345	350
	Ala Pro Cys Phe Glu Val Glu		
	355		

(97) INFORMATION FOR SEQ ID NO:95:

- 35 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 26 base pairs
 (B) TYPE: nucleic acid

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- (C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iv) ANTI-SENSE: NO

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:95:

CCCAAGCTTC CCCAGGTGTA TTTGAT

26

(97) INFORMATION FOR SEQ ID NO:96:

- 10 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 29 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iv) ANTI-SENSE: YES

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:96:

CCTGCAGGGCG AAACTGACTC TGGCTGAAG

29

(98) INFORMATION FOR SEQ ID NO:97:

- 20 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 42 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iv) ANTI-SENSE: NO

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:97:

CTGTACGCTA GTGTGTTCT ACTCACGTGT CTCAGCATTG AT

42

(99) INFORMATION FOR SEQ ID NO:98:

- 30 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 26 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

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(iv) ANTI-SENSE: YES

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:98:

GTTGGATCCA CATAATGCAT TTTCTC

26

(100) INFORMATION FOR SEQ ID NO:99:

- 5 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1080 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
- 10 (ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:99:

ATGATTCTCA ACTCTTCTAC TGAAGATGGT ATTAAAAGAA TCCAAGATGA TTGTCCAAA	60
GCTGGAAGGC ATAATTACAT ATTTGTCATG ATTCCTACTT TATACAGTAT CATCTTG TG	120
GTGGGAATAT TTGGAACACAG CTTGGTGGTG ATAGTCATTT ACTTTTATAT GAAGCTGAAG	180
15 ACTGTGGCCA GTGTTTTCT TTTGAATTAA GCACGGCTG ACTTATGCTT TTTACTGACT	240
TTGCCACTAT GGGCTGTCTA CACAGCTATG GAATACCGCT GGCCCTTTGG CAATTACCTA	300
TGTAAGATTG CTTCAGCCAG CGTCAGTTTC AACCTGTACG CTAGTGTGTT TCTACTCACG	360
TGTCTCAGCA TTGATCGATA CCTGGCTATT GTTCACCCAA TGAAGTCCCG CCTTCGACGC	420
ACAATGCTTG TAGCCAAAGT CACCTGCATC ATCATTGGC TGCTGGCAGG CTTGGCCAGT	480
20 TTGCCAGCTA TAATCCATCG AAATGTATTT TTCATTGAGA ACACCAATAT TACAGTTGT	540
GCTTTCCATT ATGAGTCCCA AAATTCAACC CTTCCGATAG GGCTGGCCT GACCAAAAT	600
ATACTGGGTT TCCTGTTCC TTTCTGATC ATTCTTACAA GTTATTTGG AATTGAAAA	660
CACTTACTGA AGACGAATAG CTATGGGAAG AACAGGATAA CCCGTGACCA AGTTAAGAAG	720
ATAATTATGG CAATTGTGCT TTTCTTTTC TTTCTGATC ATTCTTACAA GTTATTTGG AATTGAAAA	780
25 TTTCTGGATG TATTGATTCA ACTAGGCATC ATACGTGACT GTAGAATTGC AGATATTGTG	840
GACACGGCCA TGCTATCAC CATTGTATA GCTTATTTA ACAATTGCCT GAATCCTCTT	900
TTTTATGGCT TTCTGGGAA AAAATTAAA AGATATTTTC TCCAGCTTCT AAAATATATT	960
CCCCCAAAG CCAAATCCA CTCAAACCTT TCAACAAAAA TGAGCACGCT TTCCTACCGC	1020
CCCTCAGATA ATGTAAGCTC ATCCACCAAG AAGCCTGCAC CATGTTTGA GGTTGAGTGA	1080

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(101) INFORMATION FOR SEQ ID NO:100:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 359 amino acids
(B) TYPE: amino acid
5 (C) STRANDEDNESS:
(D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:100:

Met Ile Leu Asn Ser Ser Thr Glu Asp Gly Ile Lys Arg Ile Gln Asp
10 5 10 15
Asp Cys Pro Lys Ala Gly Arg His Asn Tyr Ile Phe Val Met Ile Pro
20 25 30
Thr Leu Tyr Ser Ile Ile Phe Val Val Gly Ile Phe Gly Asn Ser Leu
35 40 45
15 Val Val Ile Val Ile Tyr Phe Tyr Met Lys Leu Lys Thr Val Ala Ser
50 55 60
Val Phe Leu Leu Asn Leu Ala Leu Ala Asp Leu Cys Phe Leu Leu Thr
65 70 75 80
Leu Pro Leu Trp Ala Val Tyr Thr Ala Met Glu Tyr Arg Trp Pro Phe
20 85 90 95
Gly Asn Tyr Leu Cys Lys Ile Ala Ser Ala Ser Val Ser Phe Asn Leu
100 105 110
Tyr Ala Ser Val Phe Leu Leu Thr Cys Leu Ser Ile Asp Arg Tyr Leu
115 120 125
25 Ala Ile Val His Pro Met Lys Ser Arg Leu Arg Arg Thr Met Leu Val
130 135 140
Ala Lys Val Thr Cys Ile Ile Ile Trp Leu Leu Ala Gly Leu Ala Ser
145 150 155 160
Leu Pro Ala Ile Ile His Arg Asn Val Phe Phe Ile Glu Asn Thr Asn
30 165 170 175
Ile Thr Val Cys Ala Phe His Tyr Glu Ser Gln Asn Ser Thr Leu Pro
180 185 190
Ile Gly Leu Gly Leu Thr Lys Asn Ile Leu Gly Phe Leu Phe Pro Phe
195 200 205
35 Leu Ile Ile Leu Thr Ser Tyr Phe Gly Ile Arg Lys His Leu Leu Lys
210 215 220

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	Thr Asn Ser Tyr Gly Lys Asn Arg Ile Thr Arg Asp Gln Val Lys Lys			
	225	230	235	240
	Ile Ile Met Ala Ile Val Leu Phe Phe Phe Ser Trp Ile Pro His			
	245		250	255
5	Gln Ile Phe Thr Phe Leu Asp Val Leu Ile Gln Leu Gly Ile Ile Arg			
	260		265	270
	Asp Cys Arg Ile Ala Asp Ile Val Asp Thr Ala Met Pro Ile Thr Ile			
	275	280	285	
10	Cys Ile Ala Tyr Phe Asn Asn Cys Leu Asn Pro Leu Phe Tyr Gly Phe			
	290	295	300	
	Leu Gly Lys Lys Phe Lys Arg Tyr Phe Leu Gln Leu Leu Lys Tyr Ile			
	305	310	315	320
	Pro Pro Lys Ala Lys Ser His Ser Asn Leu Ser Thr Lys Met Ser Thr			
	325	330	335	
15	Leu Ser Tyr Arg Pro Ser Asp Asn Val Ser Ser Ser Thr Lys Lys Pro			
	340	345	350	
	Ala Pro Cys Phe Glu Val Glu			
	355			

(102) INFORMATION FOR SEQ ID NO:101:

- 20 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 37 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
- 25 (ii) MOLECULE TYPE: DNA (genomic)
- (iv) ANTI-SENSE: YES

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:101:

TCCGAATTCC AAAATAACTT GTAAGAATGA TCAGAAA

37

(103) INFORMATION FOR SEQ ID NO:102:

- 30 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 33 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
- 35 (ii) MOLECULE TYPE: DNA (genomic)
- (iv) ANTI-SENSE: NO

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:102:

AGATCTTAAG AAGATAATTAA TGGCAATTGT GCT

33

(104) INFORMATION FOR SEQ ID NO:103:

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 62 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

10 (iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:103:

AATTCGAAAA CACTTACTGA AGACGAATAG CTATGGGAAG AACAGGATAA CCCGTGACCA

60

AG

62

(105) INFORMATION FOR SEQ ID NO:104:

15 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 62 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

20 (ii) MOLECULE TYPE: DNA (genomic)

(iv) ANTI-SENSE: YES

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:104:

TTAACTTGGT CACGGGTTAT CCTGTTCTTC CCATAGCTAT TCGTCTTCAG TAAGTGTTTT

60

CG

62

25 (106) INFORMATION FOR SEQ ID NO:105:

(i) SEQUENCE CHARACTERISTICS:

- 30 (A) LENGTH: 1083 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:105:

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	ATGATTCTCA ACTCTTCTAC TGAAGATGGT ATTAAAAGAA TCCAAGATGA TTGTCCAAA	60
	GCTGGAAGGC ATAATTACAT ATTTGTCATG ATTCCTACTT TATACAGTAT CATCTTG TG	120
	GTGGGAATAT TTGGAACAG CTTGGTGGTG ATAGTCATT ACTTTTATAT GAAGCTGAAG	180
	ACTGTGGCCA GTGTTTTCT TTTGAATTAA GCACTGGCTG ACTTATGCTT TTTACTGACT	240
5	T TGCCACTAT GGGCTGTCTA CACAGCTATG GAATACCGCT GGCCCTTG CAATTACCTA	300
	TGTAAGATTG CTTCAGCCAG CGTCAGTTTC AACCTGTACG CTAGTGTGTT TCTACTCACG	360
	TGTCTCAGCA TTGATCGATA CCTGGCTATT GTTCACCCAA TGAAGTCCCG CCTTCGACGC	420
	ACAATGCTTG TAGCCAAAGT CACCTGCATC ATCATTGGC TGCTGGCAGG CTTGCCAGT	480
	TTGCCAGCTA TAATCCATCG AAATGTATTT TTCATTGAGA ACACCAATAT TACAGTTGT	540
10	GCTTTCCATT ATGAGTCCCA AAATTCAACC CTTCCGATAG GGCTGGCCT GACCAAAAT	600
	ATACTGGGTT TCCTGTTCC TTTTCTGATC ATTCTTACAA GTTATACTCT TATTTGGAAG	660
	GCCCTAAAGA AGGCTTATGA AATTAGAAG AACAAACCAA GAAATGATGA TATTTTTAAG	720
	ATAATTATGG CAGCAATTGT GCTTTCTTT TTCTTTCCCT GGATTCCCCA CCAAATATTC	780
	ACTTTCTGG ATGTATTGAT TCAACTAGGC ATCATACTG ACTGTAGAAT TGCAGATATT	840
15	GTGGACACGG CCATGCCTAT CACCATTGT ATAGCTTATT TTAACAATTG CCTGAATCCT	900
	CTTTTTATG GCTTCTGGG GAAAAAATTT AAAAGATATT TTCTCCAGCT TCTAAAATAT	960
	ATTCCCCAA AAGCCAAATC CCACTAAAC CTTCAACAA AAATGAGCAC GCTTCCTAC	1020
	CGCCCCTCAG ATAATGTAAG CTCATCCACC AAGAAGCCTG CACCATGTT TGAGGTTGAG	1080
	TGA	1083

20 (107) INFORMATION FOR SEQ ID NO:106:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 360 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:106:

Met	Ile	Leu	Asn	Ser	Ser	Thr	Glu	Asp	Gly	Ile	Lys	Arg	Ile	Gln	Asp
1															15

30 Asp Cys Pro Lys Ala Gly Arg His Asn Tyr Ile Phe Val Met Ile Pro

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	20	25	30
	Thr Leu Tyr Ser Ile Ile Phe Val Val Gly Ile Phe Gly Asn Ser Leu		
	35	40	45
5	Val Val Ile Val Ile Tyr Phe Tyr Met Lys Leu Lys Thr Val Ala Ser		
	50	55	60
	Val Phe Leu Leu Asn Leu Ala Asp Leu Cys Phe Leu Leu Thr		
	65	70	75
	Leu Pro Leu Trp Ala Val Tyr Thr Ala Met Glu Tyr Arg Trp Pro Phe		
	85	90	95
10	Gly Asn Tyr Leu Cys Lys Ile Ala Ser Ala Ser Val Ser Phe Asn Leu		
	100	105	110
	Tyr Ala Ser Val Phe Leu Leu Thr Cys Leu Ser Ile Asp Arg Tyr Leu		
	115	120	125
15	Ala Ile Val His Pro Met Lys Ser Arg Leu Arg Arg Thr Met Leu Val		
	130	135	140
	Ala Lys Val Thr Cys Ile Ile Trp Leu Leu Ala Gly Leu Ala Ser		
	145	150	155
	Leu Pro Ala Ile Ile His Arg Asn Val Phe Phe Ile Glu Asn Thr Asn		
	165	170	175
20	Ile Thr Val Cys Ala Phe His Tyr Glu Ser Gln Asn Ser Thr Leu Pro		
	180	185	190
	Ile Gly Leu Gly Leu Thr Lys Asn Ile Leu Gly Phe Leu Phe Pro Phe		
	195	200	205
25	Leu Ile Ile Leu Thr Ser Tyr Thr Leu Ile Trp Lys Ala Leu Lys Lys		
	210	215	220
	Ala Tyr Glu Ile Gln Lys Asn Lys Pro Arg Asn Asp Asp Ile Phe Lys		
	225	230	235
	Ile Ile Met Ala Ala Ile Val Leu Phe Phe Phe Ser Trp Ile Pro		
	245	250	255
30	His Gln Ile Phe Thr Phe Leu Asp Val Leu Ile Gln Leu Gly Ile Ile		
	260	265	270
	Arg Asp Cys Arg Ile Ala Asp Ile Val Asp Thr Ala Met Pro Ile Thr		
	275	280	285
35	Ile Cys Ile Ala Tyr Phe Asn Asn Cys Leu Asn Pro Leu Phe Tyr Gly		
	290	295	300
	Phe Leu Gly Lys Lys Phe Lys Arg Tyr Phe Leu Gln Leu Leu Lys Tyr		
	305	310	315
			320

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Ile Pro Pro Lys Ala Lys Ser His Ser Asn Leu Ser Thr Lys Met Ser
325 330 335

Thr Leu Ser Tyr Arg Pro Ser Asp Asn Val Ser Ser Ser Thr Lys Lys
340 345 350

5 Pro Ala Pro Cys Phe Glu Val Glu
355 360

(108) INFORMATION FOR SEQ ID NO:107:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iv) ANTI-SENSE: NO

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:107:

CCCAAGCTTC CCCAGGTGTA TTTGAT

26

(109) INFORMATION FOR SEQ ID NO:108:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 38 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iv) ANTI-SENSE: YES

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:108:

AAGCACAAATT GCTGCATAAT TATCTAAAAA ATATCATC

38

(110) INFORMATION FOR SEQ ID NO:109:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 39 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iv) ANTI-SENSE: NO

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:109:

AAGATAATTA TGGCAGCAAT TGTGCTTTTC TTTTTCTTT

39

(111) INFORMATION FOR SEQ ID NO:110:

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 26 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

10 (iv) ANTI-SENSE: YES

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:110:

GTTGGATCCA CATAATGCAT TTTCTC

26

(112) INFORMATION FOR SEQ ID NO:111:

(i) SEQUENCE CHARACTERISTICS:

- 15 (A) LENGTH: 1344 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:111:

ATGGAGCTGC TAAAGCTGAA CCGGAGCGTG CAGGGAACCG GACCCGGGCC GGGGGCTTCC

60

CTGTGCCGCC CGGGGGCGCC TCTCCTCAAC AGCAGCAGTG TGGGCAACCT CAGCTGCGAG

120

CCCCCTCGCA TTCGCGGAGC CGGGACACGA GAATTGGAGC TGGCCATTAG AATCACTCTT

180

TACGCAGTGA TCTTCCTGAT GAGCGTTGGA GGAAATATGC TCATCATCGT GGTCTGGGA

240

25 CTGAGCCGCC GCCTGAGGAC TGTCACCAAT GCCTTCCTCC TCTCACTGGC AGTCAGCGAC

300

CTCCTGCTGG CTGTGGCTTG CATGCCCTTC ACCCTCCTGC CCAATCTCAT GGGCACATTG

360

ATCTTTGGCA CCGTCATCTG CAAGGCGGTT TCCTACCTCA TGGGGGTGTC TGTGAGTGTG

420

TCCACGCTAA GCCTCGTGGC CATCGCACTG GAGCGATATA GCGCCATCTG CCGACCACCTG

480

CAGGCACGAG TGTGGCAGAC GCGCTCCCAC GCGGCTCGCG TGATTGTAGC CACGTGGCTG

540

30 CTGTCCGGAC TACTCATGGT GCCCTACCCC GTGTACACTG TCGTGCAACC AGTGGGGCCT

600

CGTGTGCTGC AGTGCAGAC TCGCTGGCCC AGTGCAGAC TCCGCCAGAC CTGGTCCGTA

660

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CTGCTGCTTC	TGCTCTTGT	TTCCATCCC	GGTGTGGTTA	TGGCCGTGGC	CTACGGGCTT	720
ATCTCTCGCG	AGCTCTACTT	AGGGCTTCGC	TTTGACGGCG	ACAGTGACAG	CGACAGCCAA	780
AGCAGGGTCC	GAAACCAAGG	CGGGCTGCCA	GGGGCTGTTC	ACCAGAACGG	GCGTTGCCGG	840
CCTGAGACTG	GCGCGGTTGG	CAAAGACAGC	GATGGCTGCT	ACGTGCAACT	TCCACGTTCC	900
5 CGGCCTGCC	TGGAGCTGAC	GGCGCTGACG	GCTCCTGGC	CGGGATCCGG	CTCCCGGCC	960
ACCCAGGCCA	AGCTGCTGGC	TAAGAACGCG	GTGAAACGAA	TGTTGCTGGT	GATCGTTGTG	1020
CTTTTTTTTC	TGTGTTGGTT	GCCAGTTAT	AGTGCCAACA	CGTGGCGCGC	CTTGATGGC	1080
CGGGGTGCAC	ACCGAGCACT	CTCGGGTGCT	CCTATCTCCT	TCATTCACTT	GCTGAGCTAC	1140
GCCTCGGCCT	GTGTCAACCC	CCTGGTCTAC	TGTTCATGC	ACCGTCGCTT	TCGCCAGGCC	1200
10 TGCCTGGAAA	CTTGCGCTCG	CTGCTGCC	CGGCCTCCAC	GAGCTGCC	CAGGGCTCTT	1260
CCCGATGAGG	ACCCTCCCAC	TCCCTCCATT	GCTTCGCTGT	CCAGGCTTAG	CTACACCACC	1320
ATCAGCACAC	TGGGCCCTGG	CTGA				1344

(113) INFORMATION FOR SEQ ID NO:112:

- 15 (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 447 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: not relevant
- (ii) MOLECULE TYPE: protein

20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:112:

Met	Glu	Leu	Leu	Lys	Leu	Asn	Arg	Ser	Val	Gln	Gly	Thr	Gly	Pro	Gly
1					5				10				15		
Pro	Gly	Ala	Ser	Leu	Cys	Arg	Pro	Gly	Ala	Pro	Leu	Leu	Asn	Ser	Ser
				20					25				30		
25 Ser	Val	Gly	Asn	Leu	Ser	Cys	Glu	Pro	Pro	Arg	Ile	Arg	Gly	Ala	Gly
				35			40			45					
Thr	Arg	Glu	Leu	Glu	Leu	Ala	Ile	Arg	Ile	Thr	Leu	Tyr	Ala	Val	Ile
				50			55			60					
30 Phe	Leu	Met	Ser	Val	Gly	Gly	Asn	Met	Leu	Ile	Ile	Val	Val	Leu	Gly
				65			70			75			80		
Leu	Ser	Arg	Arg	Leu	Arg	Thr	Val	Thr	Asn	Ala	Phe	Leu	Leu	Ser	Leu
				85			90			95					

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	Ala Val Ser Asp Leu Leu Leu Ala Val Ala Cys Met Pro Phe Thr Leu			
	100	105	110	
	Leu Pro Asn Leu Met Gly Thr Phe Ile Phe Gly Thr Val Ile Cys Lys			
	115	120	125	
5	Ala Val Ser Tyr Leu Met Gly Val Ser Val Ser Val Thr Leu Ser			
	130	135	140	
	Leu Val Ala Ile Ala Leu Glu Arg Tyr Ser Ala Ile Cys Arg Pro Leu			
	145	150	155	160
10	Gln Ala Arg Val Trp Gln Thr Arg Ser His Ala Ala Arg Val Ile Val			
	165	170	175	
	Ala Thr Trp Leu Leu Ser Gly Leu Leu Met Val Pro Tyr Pro Val Tyr			
	180	185	190	
	Thr Val Val Gln Pro Val Gly Pro Arg Val Leu Gln Cys Val His Arg			
	195	200	205	
15	Trp Pro Ser Ala Arg Val Arg Gln Thr Trp Ser Val Leu Leu Leu			
	210	215	220	
	Leu Leu Phe Phe Ile Pro Gly Val Val Met Ala Val Ala Tyr Gly Leu			
	225	230	235	240
20	Ile Ser Arg Glu Leu Tyr Leu Gly Leu Arg Phe Asp Gly Asp Ser Asp			
	245	250	255	
	Ser Asp Ser Gln Ser Arg Val Arg Asn Gln Gly Gly Leu Pro Gly Ala			
	260	265	270	
	Val His Gln Asn Gly Arg Cys Arg Pro Glu Thr Gly Ala Val Gly Lys			
	275	280	285	
25	Asp Ser Asp Gly Cys Tyr Val Gln Leu Pro Arg Ser Arg Pro Ala Leu			
	290	295	300	
	Glu Leu Thr Ala Leu Thr Ala Pro Gly Pro Gly Ser Gly Ser Arg Pro			
	305	310	315	320
30	Thr Gln Ala Lys Leu Leu Ala Lys Lys Arg Val Lys Arg Met Leu Leu			
	325	330	335	
	Val Ile Val Val Leu Phe Phe Leu Cys Trp Leu Pro Val Tyr Ser Ala			
	340	345	350	
	Asn Thr Trp Arg Ala Phe Asp Gly Pro Gly Ala His Arg Ala Leu Ser			
	355	360	365	
35	Val Ala Pro Ile Ser Phe Ile His Leu Leu Ser Tyr Ala Ser Ala Cys			
	370	375	380	
	Val Asn Pro Leu Val Tyr Cys Phe Met His Arg Arg Phe Arg Gln Ala			

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385 390 395 400

Cys Leu Glu Thr Cys Ala Arg Cys Cys Pro Arg Pro Pro Arg Ala Arg
405 410 415

5 Pro Arg Ala Leu Pro Asp Glu Asp Pro Pro Thr Pro Ser Ile Ala Ser
420 425 430

Leu Ser Arg Leu Ser Tyr Thr Thr Ile Ser Thr Leu Gly Pro Gly
435 440 445

(114) INFORMATION FOR SEQ ID NO:113:

- 10 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 34 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:113:

CAGCAGCATG CGCTTCACGC GCTTCTTAGC CCAG

34

(115) INFORMATION FOR SEQ ID NO:114:

- 20 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 33 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:114:

25 AGAAGCGCGT GAAGCGCATG CTGCTGGTGA TCGTT

35

(116) INFORMATION FOR SEQ ID NO:115:

- 30 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 33 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:115:

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ATGGAGAAAA GAATCAAAAG AATGTTCTAT ATA

33

(117) INFORMATION FOR SEQ ID NO:116:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 33 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iv) ANTI-SENSE: YES

10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:116:

TATATAGAAC ATTCTTTGA TTCTTTCTC CAT

33

(118) INFORMATION FOR SEQ ID NO:117:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iv) ANTI-SENSE: NO

20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:117:

CGCTCTCTGG CCTTGAAGCG CACGCTCAGC

30

(119) INFORMATION FOR SEQ ID NO:118:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iv) ANTI-SENSE: YES

30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:118:

GCTGAGCGTG CGCTTCAAGG CCAGAGAGCG

30

(120) INFORMATION FOR SEQ ID NO:119:

- 90 -

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 30 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
5 (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (iv) ANTI-SENSE: NO
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:119:
- CCCAGGAAAA AGGTGAAAGT CAAAGTTTC
- 10 (121) INFORMATION FOR SEQ ID NO:120:
- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 30 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
15 (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (iv) ANTI-SENSE: YES
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:120:
- GAAAACTTTG ACTTTCACCT TTTTCCTGGG
- 20 (122) INFORMATION FOR SEQ ID NO:121:
- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 27 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
25 (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (iv) ANTI-SENSE: NO
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:121:

- GGGGCGCGGG TGAAACGGCT GGTGAGC
- 30 (123) INFORMATION FOR SEQ ID NO:122:
- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 27 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single

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(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iv) ANTI-SENSE: YES

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:122:

5 GCTCACCAAGC CGTTTCACCC GCGCCCC

27

(124) INFORMATION FOR SEQ ID NO:123:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 base pairs
- (B) TYPE: nucleic acid
- 10 (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:123:

15 CCCCTTGAAA AGCCTAAGAA CTTGGTCATC

30

(125) INFORMATION FOR SEQ ID NO:124:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 base pairs
- (B) TYPE: nucleic acid
- 20 (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iv) ANTI-SENSE: YES

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:124:

25 GATGACCAAG TTCTTAGGCT TTTCAAGGGG

30

(126) INFORMATION FOR SEQ ID NO:125:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 32 base pairs
- (B) TYPE: nucleic acid
- 30 (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

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(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:125:

GATCTCTAGA ATGAAACAGCA CATGTATTGA AG

32

(127) INFORMATION FOR SEQ ID NO:126:

5 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 35 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

10 (ii) MOLECULE TYPE: DNA (genomic)

(iv) ANTI-SENSE: YES

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:126:

CTAGGGTACC CGCTCAAGGA CCTCTAACATC CATAAG

35

(128) INFORMATION FOR SEQ ID NO:127:

15 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1296 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

20 (ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:127:

ATGCAGGCCGC TTAACATTAC CCCGGAGCAG TTCTCTCGGC TGCTGCGGGGA CCACAAACCTG

60

ACGCGGGAGC AGTTCATCGC TCTGTACCGG CTGCGACCGC TCGTCTACAC CCCAGAGCTG

120

CCGGGACGCG CCAAGCTGGC CCTCGTGCTC ACCGGCGTGC TCATCTTCGC CCTGGCGCTC

180

25 TTTGGCAATG CTCTGGTGTG CTACGTGGTG ACCCGCAGCA AGGCCATGCG CACCGTCACC

240

AACATCTTTA TCTGCTCCTT GGCGCTCAGT GACCTGCTCA TCACCTTCTT CTGCATTCCC

300

GTCACCATGC TCCAGAACAT TTCCGACAAC TGGCTGGGG GTGCTTCAT TTGCAAGATG

360

GTGCCATTG TCCAGTCTAC CGCTGTTGTG ACAGAAATGC TCACTATGAC CTGCATTGCT

420

GTGGAAAGGC ACCAGGGACT TGTGCATCCT TTTAAAATGA AGTGGCAATA CACCAACCGA

480

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	AGGGCTTC CAATGCTAGG TGTGGTCTGG CTGGTGGCAG TCATCGTAGG ATCACCCATG	540
	TGGCACGTGC AACAACTTGA GATCAAATAT GACTTCCTAT ATGAAAAGGA ACACATCTGC	600
	TGCTTAGAAG AGTGGACCAG CCCTGTGCAC CAGAAGATCT ACACCACCTT CATCCTTGTC	660
	ATCCTCTTCC TCCTGCCTCT TATGGTGATG CTTATTCTGT ACAGTAAAAT TGGTTATGAA	720
5	CTTTGGATAA AGAAAAGAGT TGGGGATGGT TCAGTGCTTC GAACTATTCA TGGAAAAGAA	780
	ATGTCCAAAA TAGCCAGGAA GAAGAAACGA GCTAAGATTA TGATGGTGAC AGTGGTGGCT	840
	CTCTTGCTG TGTGCTGGC ACCATTCCAT GTTGTCCATA TGATGATTGA ATACAGTAAT	900
	TTTGAAGG AATATGATGA TGTCACAATC AAGATGATTT TTGCTATCGT GCAAATTATT	960
	GGATTTCCA ACTCCATCTG TAATCCCATT GTCTATGCAT TTATGAATGA AAACTTCAA	1020
10	AAAAATGTTT TGTCTGCAGT TTGTTATTGC ATAGTAAATA AAACCTTCTC TCCAGCACAA	1080
	AGGCATGGAA ATTCAAGGAAT TACAATGATG CGGAAGAAAG CAAAGTTTC CCTCAGAGAG	1140
	AATCCAGTGG AGGAAACCAA AGGAGAACGA TTCAGTGATG GCAACATTGA AGTCAAATTG	1200
	TGTGAACAGA CAGAGGAGAA GAAAAAGCTC AAACGACATC TTGCTCTCTT TAGGTCTGAA	1260
	CTGGCTGAGA ATTCTCCTTT AGACAGTGGG CATTAA	1296

15 (129) INFORMATION FOR SEQ ID NO:128:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 431 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 20 (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:128:

	Met Gln Ala Leu Asn Ile Thr Pro Glu Gln Phe Ser Arg Leu Leu Arg	
	1 5 10 15	
25	Asp His Asn Leu Thr Arg Glu Gln Phe Ile Ala Leu Tyr Arg Leu Arg	
	20 25 30	
	Pro Leu Val Tyr Thr Pro Glu Leu Pro Gly Arg Ala Lys Leu Ala Leu	
	35 40 45	
30	Val Leu Thr Gly Val Leu Ile Phe Ala Leu Ala Leu Phe Gly Asn Ala	
	50 55 60	
	Leu Val Phe Tyr Val Val Thr Arg Ser Lys Ala Met Arg Thr Val Thr	
	65 70 75 80	

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	Asn Ile Phe Ile Cys Ser Leu Ala Leu Ser Asp Leu Leu Ile Thr Phe			
	85	90	95	
	Phe Cys Ile Pro Val Thr Met Leu Gln Asn Ile Ser Asp Asn Trp Leu			
	100	105	110	
5	Gly Gly Ala Phe Ile Cys Lys Met Val Pro Phe Val Gln Ser Thr Ala			
	115	120	125	
	Val Val Thr Glu Met Leu Thr Met Thr Cys Ile Ala Val Glu Arg His			
	130	135	140	
10	Gln Gly Leu Val His Pro Phe Lys Met Lys Trp Gln Tyr Thr Asn Arg			
	145	150	155	160
	Arg Ala Phe Thr Met Leu Gly Val Val Trp Leu Val Ala Val Ile Val			
	165	170	175	
	Gly Ser Pro Met Trp His Val Gln Gln Leu Glu Ile Lys Tyr Asp Phe			
	180	185	190	
15	Leu Tyr Glu Lys Glu His Ile Cys Cys Leu Glu Glu Trp Thr Ser Pro			
	195	200	205	
	Val His Gln Lys Ile Tyr Thr Thr Phe Ile Leu Val Ile Leu Phe Leu			
	210	215	220	
20	Leu Pro Leu Met Val Met Leu Ile Leu Tyr Ser Lys Ile Gly Tyr Glu			
	225	230	235	240
	Leu Trp Ile Lys Lys Arg Val Gly Asp Gly Ser Val Leu Arg Thr Ile			
	245	250	255	
	His Gly Lys Glu Met Ser Lys Ile Ala Arg Lys Lys Arg Ala Lys			
	260	265	270	
25	Ile Met Met Val Thr Val Val Ala Leu Phe Ala Val Cys Trp Ala Pro			
	275	280	285	
	Phe His Val Val His Met Met Ile Glu Tyr Ser Asn Phe Glu Lys Glu			
	290	295	300	
30	Tyr Asp Asp Val Thr Ile Lys Met Ile Phe Ala Ile Val Gln Ile Ile			
	305	310	315	320
	Gly Phe Ser Asn Ser Ile Cys Asn Pro Ile Val Tyr Ala Phe Met Asn			
	325	330	335	
	Glu Asn Phe Lys Lys Asn Val Leu Ser Ala Val Cys Tyr Cys Ile Val			
	340	345	350	
35	Asn Lys Thr Phe Ser Pro Ala Gln Arg His Gly Asn Ser Gly Ile Thr			
	355	360	365	
	Met Met Arg Lys Lys Ala Lys Phe Ser Leu Arg Glu Asn Pro Val Glu			

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370 375 380

Glu Thr Lys Gly Glu Ala Phe Ser Asp Gly Asn Ile Glu Val Lys Leu
385 390 395 400

5 Cys Glu Gln Thr Glu Glu Lys Lys Lys Leu Lys Arg His Leu Ala Leu
405 410 415

Phe Arg Ser Glu Leu Ala Glu Asn Ser Pro Leu Asp Ser Gly His
420 425 430

(130) INFORMATION FOR SEQ ID NO:129:

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 2040 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:129:

ATGGGCAGCC CCTGGAACGG CAGCGACGGC CCCGAGGGGG CGCGGGAGCC GCCGTGGCCC
60

GCGCTGCCGC CTTGCGACGA GCGCCGCTGC TCGCCCTTTC CCCTGGGGGC GCTGGTGCCG
120

20 GTGACCGCTG TGTGCCGTG CCTGTTCGTC GTCGGGGTGA GCGGCAACGT GGTGACCGTG
180

ATGCTGATCG GGCGCTACCG GGACATGCGG ACCACCAACCA ACTTGTACCT GGGCAGCATG
240

25 GCCGTGTCCG ACCTACTCAT CCTGCTCGGG CTGCCGTTCG ACCTGTACCG CCTCTGGCGC
300

TCGCAGCCCT GGGTGTTCGG GCCGCTGCTC TGCCGCCTGT CCCTCTACGT GGGCGAGGGC
360

30 TGCACCTACG CCACGCTGCT GCACATGACC GCGCTCAGCG TCGAGCGCTA CCTGGCCATC
420

TGCCGCCCGC TCCGCGCCCG CGTCTTGGTC ACCCGGGGCC GCGTCCGCGC GCTCATCGCT
480

35 GTGCTCTGGG CCGTGGCGCT GCTCTCTGCC GGTCCCTTCT TGTTCCGTG GTGGCGTCGAG
540

CAGGACCCCG GCATCTCCGT AGTCCCAGGC CTCAATGGCA CCGCGCGGAT CGCCTCCTCG
600

40 CCTCTCGCCT CGTCGCCGCC TCTCTGGCTC TCGCGGGCGC CACCGCCGTC CCCGCCGTG

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660
GGGCCCGAGA CCGCGGAGGC CGCGGCGCTG TTCAGCCGCG AATGCCGCC GAGCCCCGCG
720
5 CAGCTGGCG CGCTGCGTGT CATGCTGTGG GTCACCACCG CCTACTTCTT CCTGCCCTTT
780
CTGTGCCTCA GCATCCTCTA CGGGCTCATC GGGCGGGAGC TGTGGAGCAG CCGGCAGGCCG
10 840
CTGCGAGGCC CGGCCGCCTC GGGGCGGGAG AGAGGCCACC GGCAGACCAA ACGCGTCCTG
900
15 CGTAAGTGGA GCCGCCGTGG TTCCAAAGAC GCCTGCCTGC AGTCCGCCCG GCCGGGGACC
960
GCGCAAACGC TGGGTCCCCT TCCCCTGCTC GCCCAGCTCT GGGCGCCGCT TCCAGCTCCC
1020
20 TTTCCTATTG CGATTCCAGC CTCCACCCGC CGGTACTTCC CATCCCCGA GAAAACCATG
1080
TCCTGTCCCC CAGGAGCTCT GGGGGACCCC AGGGCGCTTT GAGGGTGGGA TCCCCGGATC
25 1140
CGATTCAAGTA ACCAGCAGTG CTTTTCCAGA GCCTCTGAGA CCAGAAAGGA GAGTTGGTAA
1200
30 TTCTTAATCC AACCACCTGT TAGATGCCAC AAATGAGGAG TCCTCACAGT GCTCTTGAGA
1260
AGACGAGGGA GATTCATTA AGCTAAAATT TTTTATTTAA TGTAAAGTGA TGCTGAAGGC
1320
35 TAAAGTAAAC CTTGCTCGTA TCAAAAAGTA AAGATTGTGC AGACCTGTTG TAGAATTCTT
1380
TTCAACAGAG AACAGAAAAC TTGTCTCCGA AGTGGGTTTG TGGAAGGAAG CCTGCCAAGG
40 1440
CGGCTTGTTC AGAGAAATTG CTCCTTCTGG TTTATGTCCA GCCTTGATAA CACATATGGG
1500
45 AGCCTACTAT GCAGTTTAA AGCAAGTATC CATGCAGCCT GCAGCCTGGT CATTTCCTTCT
1560
GGGGTGAGGA TCTGCCTAGG TAGAAGTTTT CTCTAATTAA TTTTGCTGTT ACTTGTTATT
1620
50 GCAGATGGTT CCTTGTCGGG GTGGGGGGTT TATTTGCTTC CCAATGCTTT TGTAAATCCC
1680
55 GGTGCTGTGT CTTATGTTGC AGTGGTGGTG GTTCTGGCAT TTATAATTG CTGGTTGCC
1740

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TTCCACGTTG GCAGAACAT TTACATAAAC ACGGAAGATT CGCGGATGAT GTACTTCTCT
1800

5 CAGTACTTTA ACATCGTCGC TCTGCAACTT TTCTATCTGA GCGCATCTAT CAACCCAATC
1860

CTCTACAACC TCATTTCAAA GAAGTACAGA GCGGCAGCCT TTAAACTGCT GCTCGCAAGG
1920

10 AAGTCCAGGC CGAGAGGCTT CCACAGAACG AGGGACACTG CGGGGGAAAGT TGCAGGGGAC
1980

15 ACTGGAGGAG ACACGGTGGG CTACACCGAG ACAAGCGCTA ACGTGAAGAC GATGGGATAA
2040

(131) INFORMATION FOR SEQ ID NO:130:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 412 amino acids
- (B) TYPE: amino acid
- 20 (C) STRANDEDNESS:
- (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:130:

Met Gly Ser Pro Trp Asn Gly Ser Asp Gly Pro Glu Gly Ala Arg Glu
25 1 5 10 15

Pro Pro Trp Pro Ala Leu Pro Pro Cys Asp Glu Arg Arg Cys Ser Pro
20 25 30

Phe Pro Leu Gly Ala Leu Val Pro Val Thr Ala Val Cys Leu Cys Leu
35 40 45

30 Phe Val Val Gly Val Ser Gly Asn Val Val Thr Val Met Leu Ile Gly
50 55 60

Arg Tyr Arg Asp Met Arg Thr Thr Asn Leu Tyr Leu Gly Ser Met
65 70 75 80

Ala Val Ser Asp Leu Leu Ile Leu Gly Leu Pro Phe Asp Leu Tyr
35 85 90 95

Arg Leu Trp Arg Ser Arg Pro Trp Val Phe Gly Pro Leu Leu Cys Arg
100 105 110

Leu Ser Leu Tyr Val Gly Glu Gly Cys Thr Tyr Ala Thr Leu Leu His
115 120 125

40 Met Thr Ala Leu Ser Val Glu Arg Tyr Leu Ala Ile Cys Arg Pro Leu
130 135 140

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	Arg Ala Arg Val Leu Val Thr Arg Arg Arg Val Arg Ala Leu Ile Ala			
	145	150	155	160
	Val Leu Trp Ala Val Ala Leu Leu Ser Ala Gly Pro Phe Leu Phe Leu			
	165	170		175
5	Val Gly Val Glu Gln Asp Pro Gly Ile Ser Val Val Pro Gly Leu Asn			
	180	185		190
	Gly Thr Ala Arg Ile Ala Ser Ser Pro Leu Ala Ser Ser Pro Pro Leu			
	195	200		205
10	Trp Leu Ser Arg Ala Pro Pro Ser Pro Pro Ser Gly Pro Glu Thr			
	210	215		220
	Ala Glu Ala Ala Ala Leu Phe Ser Arg Glu Cys Arg Pro Ser Pro Ala			
	225	230	235	240
	Gln Leu Gly Ala Leu Arg Val Met Leu Trp Val Thr Thr Ala Tyr Phe			
	245	250		255
15	Phe Leu Pro Phe Leu Cys Leu Ser Ile Leu Tyr Gly Leu Ile Gly Arg			
	260	265		270
	Glu Leu Trp Ser Ser Arg Arg Pro Leu Arg Gly Pro Ala Ala Ser Gly			
	275	280		285
20	Arg Glu Arg Gly His Arg Gln Thr Lys Arg Val Leu Leu Val Val Val			
	290	295		300
	Leu Ala Phe Ile Ile Cys Trp Leu Pro Phe His Val Gly Arg Ile Ile			
	305	310	315	320
	Tyr Ile Asn Thr Glu Asp Ser Arg Met Met Tyr Phe Ser Gln Tyr Phe			
	325	330		335
25	Asn Ile Val Ala Leu Gln Leu Phe Tyr Leu Ser Ala Ser Ile Asn Pro			
	340	345		350
	Ile Leu Tyr Asn Leu Ile Ser Lys Lys Tyr Arg Ala Ala Phe Lys			
	355	360		365
30	Leu Leu Leu Ala Arg Lys Ser Arg Pro Arg Gly Phe His Arg Ser Arg			
	370	375		380
	Asp Thr Ala Gly Glu Val Ala Gly Asp Thr Gly Gly Asp Thr Val Gly			
	385	390	395	400
	Tyr Thr Glu Thr Ser Ala Asn Val Lys Thr Met Gly			
	405	410		

35 (132) INFORMATION FOR SEQ ID NO:131:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1344 base pairs

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- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:131:

ATGGAGCTGC TAAAGCTGAA CGGGAGCGTG CAGGGAACCG GACCCGGGCC GGGGGCTTCC
60CTGTGCCGCC CGGGGGCGCC TCTCCTCAAC AGCAGCAGTG TGGGCAACCT CAGCTGCGAG
12010 CCCCTCGCA TTCGCGGAGC CGGGACACGA GAATTGGAGC TGGCCATTAG AATCACTCTT
180TACGCAGTGA TCTTCCTGAT GAGCGTTGGA GGAAATATGC TCATCATCGT GGTCTGGGA
24015 CTGAGCCGCC GCCTGAGGAC TGTCACCAAT GCCTTCCTCC TCTCACTGGC AGTCAGCGAC
300CTCCTGCTGG CTGTGGCTTG CATGCCCTTC ACCCTCCTGC CCAATCTCAT GGGCACATTG
360ATCTTGCA CCGTCATCTG CAAGGCGGTT TCCTACCTCA TGGGGGTGTC TGTGAGTGTG
42020 TCCACGCTAA GCCTCGTGGC CATCGCACTG GAGCGATATA GCGCCATCTG CCGACCACGT
480CAGGCACGAG TGTGGCAGAC GCGCTCCCAC GCGGCTCGCG TGATTGTAGC CACGTGGCTG
54025 CTGTCCGGAC TACTCATGGT GCCCTACCCC GTGTACACTG TCGTGCAACC AGTGGGGCCT
600CGTGTGCTGC AGTGCCTGCA TCGCTGGCCC AGTGCCTGGG TCCGCCAGAC CTGGTCCGTA
660CTGCTGCTTC TGCTCTTGTGTT CTTCATCCCA GGTGTGGTTA TGGCCGTGGC CTACGGGCTT
72030 ATCTCTCGCG AGCTCTACTT AGGGCTTCGC TTTGACGGCG ACAGTGACAG CGACAGCCAA
780AGCAGGGTCC GAAACCAAGG CGGGCTGCCA GGGGCTGTTC ACCAGAACGG CGGTTGCCGG
84035 CCTGAGACTG GCGCGGTTGG CAAAGACAGC GATGGCTGCT ACAGTGCAACT TCCACGTTCC
900

CGGCCTGCC CGGGCTGCCA GGGGATCCGG CTCCCGGCC

- 100 -

960

ACCCAGGCCA AGCTGCTGGC TAAGAACGAA GTGAAACGAA TGTTGCTGGT GATCGTTGTG
1020

5 CTTTTTTTTC TGTGTTGGTT GCCAGTTAT AGTGCCAACA CGTGGCGCGC CTTTGATGGC
1080

CCGGGTGCAC ACCGAGCACT CTCGGGTGCT CCTATCTCCT TCATTCAC TT GCTGAGCTAC
1140

GCCTCGGCCT GTGTCAAACCC CCTGGTCTAC TGCTTCATGC ACCGTCGCTT TCGCCAGGCC
1200

10 TGCCCTGGAAA CTTGCGCTCG CTGCTGCCCC CGGCCTCCAC GAGCTGCCCC CAGGGCTCTT
1260

CCCGATGAGG ACCCTCCCAC TCCCTCCATT GCTTCGCTGT CCAGGGCTTAG CTACACCACC
1320

15 ATCAGCACAC TGGGCCCTGG CTGA
1344

(133) INFORMATION FOR SEQ ID NO:132:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 447 amino acids
- (B) TYPE: amino acid
- 20 (C) STRANDEDNESS:
- (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:132:

25 Met Glu Leu Leu Lys Leu Asn Arg Ser Val Gln Gly Thr Gly Pro Gly
1 5 10 15

Pro Gly Ala Ser Leu Cys Arg Pro Gly Ala Pro Leu Leu Asn Ser Ser
20 25 30

Ser Val Gly Asn Leu Ser Cys Glu Pro Pro Arg Ile Arg Gly Ala Gly
35 40 45

30 Thr Arg Glu Leu Glu Leu Ala Ile Arg Ile Thr Leu Tyr Ala Val Ile
50 55 60

Phe Leu Met Ser Val Gly Asn Met Leu Ile Ile Val Val Leu Gly
65 70 75 80

35 Leu Ser Arg Arg Leu Arg Thr Val Thr Asn Ala Phe Leu Leu Ser Leu
85 90 95

Ala Val Ser Asp Leu Leu Ala Val Ala Cys Met Pro Phe Thr Leu

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	100	105	110
	Leu Pro Asn Leu Met Gly Thr Phe Ile Phe Gly Thr Val Ile Cys Lys		
	115	120	125
5	Ala Val Ser Tyr Leu Met Gly Val Ser Val Ser Val Ser Thr Leu Ser		
	130	135	140
	Leu Val Ala Ile Ala Leu Glu Arg Tyr Ser Ala Ile Cys Arg Pro Leu		
	145	150	155
	Gln Ala Arg Val Trp Gln Thr Arg Ser His Ala Ala Arg Val Ile Val		
	165	170	175
10	Ala Thr Trp Leu Leu Ser Gly Leu Leu Met Val Pro Tyr Pro Val Tyr		
	180	185	190
	Thr Val Val Gln Pro Val Gly Pro Arg Val Leu Gln Cys Val His Arg		
	195	200	205
15	Trp Pro Ser Ala Arg Val Arg Gln Thr Trp Ser Val Leu Leu Leu Leu		
	210	215	220
	Leu Leu Phe Phe Ile Pro Gly Val Val Met Ala Val Ala Tyr Gly Leu		
	225	230	235
	Ile Ser Arg Glu Leu Tyr Leu Gly Leu Arg Phe Asp Gly Asp Ser Asp		
	245	250	255
20	Ser Asp Ser Gln Ser Arg Val Arg Asn Gln Gly Gly Leu Pro Gly Ala		
	260	265	270
	Val His Gln Asn Gly Arg Cys Arg Pro Glu Thr Gly Ala Val Gly Lys		
	275	280	285
25	Asp Ser Asp Gly Cys Tyr Val Gln Leu Pro Arg Ser Arg Pro Ala Leu		
	290	295	300
	Glu Leu Thr Ala Leu Thr Ala Pro Gly Pro Gly Ser Gly Ser Arg Pro		
	305	310	315
	320		
	Thr Gln Ala Lys Leu Leu Ala Lys Lys Arg Val Lys Arg Met Leu Leu		
	325	330	335
30	Val Ile Val Val Leu Phe Phe Leu Cys Trp Leu Pro Val Tyr Ser Ala		
	340	345	350
	Asn Thr Trp Arg Ala Phe Asp Gly Pro Gly Ala His Arg Ala Leu Ser		
	355	360	365
35	Val Ala Pro Ile Ser Phe Ile His Leu Leu Ser Tyr Ala Ser Ala Cys		
	370	375	380
	Val Asn Pro Leu Val Tyr Cys Phe Met His Arg Arg Phe Arg Gln Ala		
	385	390	395
	400		

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Cys	Leu	Glu	Thr	Cys	Ala	Arg	Cys	Cys	Pro	Arg	Pro	Pro	Arg	Ala	Arg
				405					410					415	
Pro	Arg	Ala	Leu	Pro	Asp	Glu	Asp	Pro	Pro	Thr	Pro	Ser	Ile	Ala	Ser
	420						425						430		
Leu	Ser	Arg	Leu	Ser	Tyr	Thr	Thr	Ile	Ser	Thr	Leu	Gly	Pro	Gly	
	435					440						445			

(134) INFORMATION FOR SEQ ID NO:133:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1014 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:133:

15	ATGAACAGCA CATGTATTGA AGAACAGCAT GACCTGGATC ACTATTGTT TCCCATTGTT TACATCTTG TGATTATAAGT CAGCATTCCA GCCAATATTG GATCTCTGTG TGTGTCTTC CTGCAAGCAA AGAAGGAAAG TGAACCTAGGA ATTACCTCT TCAGTTGTC ACTATCAGAT TTACTCTATG CATTAACACTCT CCCTTTATGG ATTGATTATA CTTGGAATAA AGACAACCTGG ACTTTCTCTC CTGCCTTGTG CAAAGGGAGT GCTTTCTCA TGTACATGAA TTTTTACAGC	600 120 180 240 300
20	AGCACAGCAT TCCTCACCTG CATTGCCGTT GATCGGTATT TGGCTGTTGT CTACCCTTG AAGTTTTTT TCCTAAGGAC AAGAAGATT GCACTCATGG TCAGCCTGTC CATCTGGATA TTGGAAACCA TCTTCAATGC TGTCACTGTTG TGGGAAGATG AAACAGTTGT TGAATATTGC GATGCCGAAA AGTCTAATT TACTTTATGC TATGACAAAT ACCCTTAGA GAAATGGCAA ATCAACCTCA ACTTGTTCAAG GACGTGTACA GGCTATGCAA TACCTTGTT CACCACCTG	360 420 480 540 600
25	ATCTGTAACC GGAAAGTCTA CCAAGCTGTG CGGCACAATA AAGCCACGGA AAACAAGGAA AAGAAGAGAA TCAAAAAACT ACTTGTCAGC ATCACAGTTA CTTTTGTCTT ATGCTTTACT CCCTTCATG TGATGTTGCT GATTGCTGC ATTTTAGAGC ATGCTGTGAA CTTCGAAGAC CACAGCAATT CTGGGAAGCG AACTTACACA ATGTATAGAA TCACGGTTGC ATTAACAAGT TTAAATTGTTG TTGCTGATCC AATTCTGTAC TGTTTGTTA CCGAAACAGG AAGATATGAT	660 720 780 840 900
30	ATGTGGAATA TATTAAAATT CTGCACTGGG AGGTGTAATA CATCACAAAG ACAAAAGAAAA CGCATACTTT CTGTGTCTAC AAAAGATACT ATGGAATTAG AGGTCCCTGAA GTAG	960 1014

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(135) INFORMATION FOR SEQ ID NO:134:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 337 amino acids
 - (B) TYPE: amino acid
 - 5 (C) STRANDEDNESS:
 - (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:134:

	Met Asn Ser Thr Cys Ile Glu Glu Gln His Asp Leu Asp His Tyr Leu	
10	1 5 10 15	
	Phe Pro Ile Val Tyr Ile Phe Val Ile Ile Val Ser Ile Pro Ala Asn	
	20 25 30	
	Ile Gly Ser Leu Cys Val Ser Phe Leu Gln Ala Lys Lys Glu Ser Glu	
	35 40 45	
15	Leu Gly Ile Tyr Leu Phe Ser Leu Ser Leu Ser Asp Leu Leu Tyr Ala	
	50 55 60	
	Leu Thr Leu Pro Leu Trp Ile Asp Tyr Thr Trp Asn Lys Asp Asn Trp	
	65 70 75 80	
20	Thr Phe Ser Pro Ala Leu Cys Lys Gly Ser Ala Phe Leu Met Tyr Met	
	85 90 95	
	Asn Phe Tyr Ser Ser Thr Ala Phe Leu Thr Cys Ile Ala Val Asp Arg	
	100 105 110	
	Tyr Leu Ala Val Val Tyr Pro Leu Lys Phe Phe Phe Leu Arg Thr Arg	
	115 120 125	
25	Arg Phe Ala Leu Met Val Ser Leu Ser Ile Trp Ile Leu Glu Thr Ile	
	130 135 140	
	Phe Asn Ala Val Met Leu Trp Glu Asp Glu Thr Val Val Glu Tyr Cys	
	145 150 155 160	
30	Asp Ala Glu Lys Ser Asn Phe Thr Leu Cys Tyr Asp Lys Tyr Pro Leu	
	165 170 175	
	Glu Lys Trp Gln Ile Asn Leu Asn Leu Phe Arg Thr Cys Thr Gly Tyr	
	180 185 190	
	Ala Ile Pro Leu Val Thr Ile Leu Ile Cys Asn Arg Lys Val Tyr Gln	
	195 200 205	
35	Ala Val Arg His Asn Lys Ala Thr Glu Asn Lys Glu Lys Lys Arg Ile	
	210 215 220	

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Lys Lys Leu Leu Val Ser Ile Thr Val Thr Phe Val Leu Cys Phe Thr
225 230 235 240

Pro Phe His Val Met Leu Leu Ile Arg Cys Ile Leu Glu His Ala Val
245 250 255

5 Asn Phe Glu Asp His Ser Asn Ser Gly Lys Arg Thr Tyr Thr Met Tyr
260 265 270

Arg Ile Thr Val Ala Leu Thr Ser Leu Asn Cys Val Ala Asp Pro Ile
275 280 285

10 Leu Tyr Cys Phe Val Thr Glu Thr Gly Arg Tyr Asp Met Trp Asn Ile
290 295 300

Leu Lys Phe Cys Thr Gly Arg Cys Asn Thr Ser Gln Arg Gln Arg Lys
305 310 315 320

Arg Ile Leu Ser Val Ser Thr Lys Asp Thr Met Glu Leu Glu Val Leu
325 330 335

15 Glu

(136) INFORMATION FOR SEQ ID NO:135:

- (i) SEQUENCE CHARACTERISTICS:
- 20 (A) LENGTH: 999 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:135:

25 ATGGTGAAC CCACCCACCG TGGGATGCAC ACTTCTCTGC ACCTCTGGAA CCGCAGCAGT
60

TACAGACTGC ACAGCAATGC CAGTGAGTCC CTTGGAAAAG GCTACTCTGA TGGAGGGTGC
120

30 TACGAGCAAC TTTTGTCCTC TCCTGAGGTG TTTGTGACTC TGGGTGTCAT CAGCTTGTG
180

GAGAATATCT TAGTGATTGT GGCAATAGCC AAGAACAAAGA ATCTGCATTC ACCCATGTAC
240

TTTTTCATCT GCAGCTTGGC TGTGGCTGAT ATGCTGGTGA GCGTTCAAA TGGATCAGAA
300

35 ACCATTATCA TCACCCTATT AAACAGTACA GATACTGGATG CACAGAGTTT CACAGTGAAT
360

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ATTGATAATG TCATTGACTC GGTGATCTGT AGCTCCTTGC TTGCATCCAT TTGCAGCCTG
420

CTTCAATTG CAGTGGACAG GTACTTTACT ATCTTCTATG CTCTCCAGTA CCATAACATT
480

5 ATGACAGTTA AGCGGGTTGG GATCAGCATA AGTTGTATCT GGGCAGCTTG CACGGTTCA
540

GGCATTGT TCATCATTAA CTCAGATAGT AGTGCTGTCA TCATCTGCCT CATCACCATG
600

10 TTCTCACCA TGCTGGCTCT CATGGCTTCT CTCTATGTCC ACATGTTCC GATGCCAGG
660

CTTCACATTA AGAGGATTGC TGCCTCCCC GGCAGTGGTG CCATCCGCCA AGGTGCCAAT
720

ATGAAGGGAA AAATTACCTT GACCATCCTG ATTGGCGTCT TTGTTGTCTG CTGGGCCCA
780

15 TTCTCCTCC ACTTAATATT CTACATCTCT TGTCTCAGA ATCCATATTG TGTGTGCTTC
840

ATGTCTCACT TTAACTTGTA TCTCATACTG ATCATGTGTA ATTCAATCAT CGATCCTCTG
900

20 ATTTATGCAC TCCGGAGTCA AGAACTGAGG AAAACCTTCA AAGAGATCAT CTGTTGCTAT
960

CCCCTGGGAG GCCTTGTGA CTTGTCTAGC AGATATTAA
999

(137) INFORMATION FOR SEQ ID NO:136:

(i) SEQUENCE CHARACTERISTICS:

- 25 (A) LENGTH: 332 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: protein

30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:136:

Met Val Asn Ser Thr His Arg Gly Met His Thr Ser Leu His Leu Trp
1 5 10 15

Asn Arg Ser Ser Tyr Arg Leu His Ser Asn Ala Ser Glu Ser Leu Gly
20 25 30

35 Lys Gly Tyr Ser Asp Gly Gly Cys Tyr Glu Gln Leu Phe Val Ser Pro
35 40 45

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Glu Val Phe Val Thr Leu Gly Val Ile Ser Leu Leu Glu Asn Ile Leu
50 55 60

Val Ile Val Ala Ile Ala Lys Asn Lys Asn Leu His Ser Pro Met Tyr
65 70 75 80

5 Phe Phe Ile Cys Ser Leu Ala Val Ala Asp Met Leu Val Ser Val Ser
85 90 95

Asn Gly Ser Glu Thr Ile Ile Thr Leu Leu Asn Ser Thr Asp Thr
100 105 110

Asp Ala Gln Ser Phe Thr Val Asn Ile Asp Asn Val Ile Asp Ser Val
10 115 120 125

Ile Cys Ser Ser Leu Leu Ala Ser Ile Cys Ser Leu Leu Ser Ile Ala
130 135 140

Val Asp Arg Tyr Phe Thr Ile Phe Tyr Ala Leu Gln Tyr His Asn Ile
145 150 155 160

15 Met Thr Val Lys Arg Val Gly Ile Ser Ile Ser Cys Ile Trp Ala Ala
165 170 175

Cys Thr Val Ser Gly Ile Leu Phe Ile Ile Tyr Ser Asp Ser Ser Ala
180 185 190

Val Ile Ile Cys Leu Ile Thr Met Phe Phe Thr Met Leu Ala Leu Met
20 195 200 205

Ala Ser Leu Tyr Val His Met Phe Leu Met Ala Arg Leu His Ile Lys
210 215 220

Arg Ile Ala Val Leu Pro Gly Thr Gly Ala Ile Arg Gln Gly Ala Asn
225 230 235 240

25 Met Lys Gly Lys Ile Thr Leu Thr Ile Leu Ile Gly Val Phe Val Val
245 250 255

Cys Trp Ala Pro Phe Phe Leu His Leu Ile Phe Tyr Ile Ser Cys Pro
260 265 270

Gln Asn Pro Tyr Cys Val Cys Phe Met Ser His Phe Asn Leu Tyr Leu
30 275 280 285

Ile Leu Ile Met Cys Asn Ser Ile Ile Asp Pro Leu Ile Tyr Ala Leu
290 295 300

Arg Ser Gln Glu Leu Arg Lys Thr Phe Lys Glu Ile Ile Cys Cys Tyr
305 310 315 320

35 Pro Leu Gly Gly Leu Cys Asp Leu Ser Ser Arg Tyr
325 330

(138) INFORMATION FOR SEQ ID NO:137:

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- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 33 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
5 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:137:

GCCAAATATGA AGGGAAAAAT TACCTTGACC ATC
33

10 (137) INFORMATION FOR SEQ ID NO:138:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 31 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
15 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:138:

CTCCTTCGGT CCTCCTATCG TTGTCAGAAG T
31

20 (140) INFORMATION FOR SEQ ID NO:139:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1842 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
25 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:139:

ATGGGGCCCA CCCTAGCGGT TCCCACCCCC TATGGCTGTA TTGGCTGTAA GCTACCCCAG	60
CCAGAATACC CACCGGCTCT AATCATCTTT ATGTTCTGCG CGATGGTTAT CACCATCGTT	120
30 GTAGACCTAA TCGGCAACTC CATGGTCATT TTGGCTGTGA CGAAGAACAA GAAGCTCCGG	180
AATTCTGGCA ACATCTTCGT GGTCAGTCTC TCTGTGGCCG ATATGCTGGT GGCCATCTAC	240
CCATACCCTT TGATGCTGCA TGCCATGTCC ATTGGGGCT GGGATCTGAG CCAGTTACAG	300
TGCCAGATGG TCGGGTTCAT CACAGGGCTG AGTGTGGTCG GCTCCATCTT CAACATCGTG	360

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GCAATCGCTA	TCAACCGTTA	CTGCTACATC	TGCCACAGCC	TCCAGTACGA	ACGGATCTTC	420
AGTGTGCGCA	ATACCTGCAT	CTACCTGGTC	ATCACCTGGA	TCATGACCGT	CCTGGCTGTC	480
CTGCCCAACA	TGTACATTGG	CACCATCGAG	TACGATCCTC	GCACCTACAC	CTGCATCTTC	540
AACTATCTGA	ACAACCCTGT	CTTCACTGTT	ACCATCGTCT	GCATCCACTT	CGTCCTCCCT	600
5	CTCCTCATCG	TGGGTTTCTG	CTACGTGAGG	ATCTGGACCA	AAGTGCTGGC	GGCCC GTGAC
	CCTGCAGGGC	AGAACCTGA	CAACCAACTT	GCTGAGGTTC	GCAATTTC	720
	GTGATCTTCC	TCCTCTTGC	AGTGTGCTGG	TGCCCTATCA	ACGTGCTCAC	TGTCTTGGTG
	GCTGTCAGTC	CGAAGGAGAT	GGCAGGCAAG	ATCCCCACT	GGCTTTATCT	TGCAGCCTAC
	TTCATAGCCT	ACTTCAACAG	CTGCCTCAAC	GCTGTGATCT	ACGGGCTCCT	CAATGAGAAT
10	TTCCGAAGAG	AATACTGGAC	CATCTTCAT	GCTATGCGGC	ACCCTATCAT	ATTCTTCCCT
	GGCCTCATCA	GTGATATTG	TGAGATGCAG	GAGGCCCGTA	CCCTGGCCCG	CGCCCGTGCC
	CATGCTCGCG	ACCAAGCTCG	TGAACAAGAC	CGTGCCCATG	CCTGCTCTGC	TGTGGAGGAA
	ACCCCGATGA	ATGTCCGGAA	TGTTCCATTA	CCTGGTGATG	CTGCAGCTGG	CCACCCCGAC
	CGTGCCTCTG	GCCACCCCTAA	GCCCCATTCC	AGATCCTCCT	CTGCCTATCG	CAAATCTGCC
15	TCTACCCACC	ACAAGTCTGT	CTTAGCCAC	TCCAAGGCTG	CCTCTGGTCA	CCTCAAGCCT
	GTCTCTGGCC	ACTCCAAGCC	TGCCTCTGGT	CACCCCAAGT	CTGCCACTGT	CTACCCCTAAG
	CCTGCCTCTG	TCCATTCAA	GGGTGACTCT	GTCCATTCA	AGGGTGACTC	TGTCCATTTC
	AAGCCTGACT	CTGTTCATTT	CAAGCCTGCT	TCCAGCAACC	CCAAGCCCAT	CACTGGCCAC
	CATGTCTCTG	CTGGCAGCCA	CTCCAAGTCT	GCCTTCAGTG	CTGCCACCAG	CCACCCCTAAA
20	CCCATCAAGC	CAGCTACCAAG	CCATGCTGAG	CCCACCACTG	CTGACTATCC	CAAGCCTGCC
	ACTACCAGCC	ACCCTAACGCC	CGCTGCTGCT	GACAACCCCTG	AGCTCTCTGC	CTCCCATTGC
	CCCGAGATCC	CTGCCATTGC	CCACCCCTGTG	TCTGACGACA	GTGACCTCCC	TGAGTCGGCC
	TCTAGCCCTG	CCGCTGGGCC	CACCAAGCCT	GCTGCCAGCC	AGCTGGAGTC	TGACACCATC
	GCTGACCTTC	CTGACCCCTAC	TGTAGTCACT	ACCAGTACCA	ATGATTACCA	TGATGTCGTG
25	GTTGTTGATG	TTGAAGATGA	TCCTGATGAA	ATGGCTGTGT	GA	1842

(141) INFORMATION FOR SEQ ID NO:140:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 613 amino acids
 - (B) TYPE: amino acid

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(C) STRANDEDNESS:
(D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:140:

5	Met Gly Pro Thr Leu Ala Val Pro Thr Pro Tyr Gly Cys Ile Gly Cys 1 5 10 15
	Lys Leu Pro Gln Pro Glu Tyr Pro Pro Ala Leu Ile Ile Phe Met Phe 20 25 30
10	Cys Ala Met Val Ile Thr Ile Val Val Asp Leu Ile Gly Asn Ser Met 35 40 45
	Val Ile Leu Ala Val Thr Lys Asn Lys Lys Leu Arg Asn Ser Gly Asn 50 55 60
	Ile Phe Val Val Ser Leu Ser Val Ala Asp Met Leu Val Ala Ile Tyr 65 70 80
15	Pro Tyr Pro Leu Met Leu His Ala Met Ser Ile Gly Gly Trp Asp Leu 85 90 95
	Ser Gln Leu Gln Cys Gln Met Val Gly Phe Ile Thr Gly Leu Ser Val 100 105 110
20	Val Gly Ser Ile Phe Asn Ile Val Ala Ile Ala Ile Asn Arg Tyr Cys 115 120 125
	Tyr Ile Cys His Ser Leu Gln Tyr Glu Arg Ile Phe Ser Val Arg Asn 130 135 140
	Thr Cys Ile Tyr Leu Val Ile Thr Trp Ile Met Thr Val Leu Ala Val 145 150 160
25	Leu Pro Asn Met Tyr Ile Gly Thr Ile Glu Tyr Asp Pro Arg Thr Tyr 165 170 175
	Thr Cys Ile Phe Asn Tyr Leu Asn Asn Pro Val Phe Thr Val Thr Ile 180 185 190
30	Val Cys Ile His Phe Val Leu Pro Leu Leu Ile Val Gly Phe Cys Tyr 195 200 205
	Val Arg Ile Trp Thr Lys Val Leu Ala Ala Arg Asp Pro Ala Gly Gln 210 215 220
	Asn Pro Asp Asn Gln Leu Ala Glu Val Arg Asn Phe Leu Thr Met Phe 225 230 240
35	Val Ile Phe Leu Leu Phe Ala Val Cys Trp Cys Pro Ile Asn Val Leu 245 250 255

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	Thr Val Leu Val Ala Val Ser Pro Lys Glu Met Ala Gly Lys Ile Pro			
	260	265	270	
	Asn Trp Leu Tyr Leu Ala Ala Tyr Phe Ile Ala Tyr Phe Asn Ser Cys			
	275	280	285	
5	Leu Asn Ala Val Ile Tyr Gly Leu Leu Asn Phe Arg Arg Glu			
	290	295	300	
	Tyr Trp Thr Ile Phe His Ala Met Arg His Pro Ile Ile Phe Phe Pro			
	305	310	315	320
10	Gly Leu Ile Ser Asp Ile Arg Glu Met Gln Glu Ala Arg Thr Leu Ala			
	325	330	335	
	Arg Ala Arg Ala His Ala Arg Asp Gln Ala Arg Glu Gln Asp Arg Ala			
	340	345	350	
	His Ala Cys Pro Ala Val Glu Glu Thr Pro Met Asn Val Arg Asn Val			
	355	360	365	
15	Pro Leu Pro Gly Asp Ala Ala Gly His Pro Asp Arg Ala Ser Gly			
	370	375	380	
	His Pro Lys Pro His Ser Arg Ser Ser Ser Ala Tyr Arg Lys Ser Ala			
	385	390	395	400
20	Ser Thr His His Lys Ser Val Phe Ser His Ser Lys Ala Ala Ser Gly			
	405	410	415	
	His Leu Lys Pro Val Ser Gly His Ser Lys Pro Ala Ser Gly His Pro			
	420	425	430	
	Lys Ser Ala Thr Val Tyr Pro Lys Pro Ala Ser Val His Phe Lys Gly			
	435	440	445	
25	Asp Ser Val His Phe Lys Gly Asp Ser Val His Phe Lys Pro Asp Ser			
	450	455	460	
	Val His Phe Lys Pro Ala Ser Ser Asn Pro Lys Pro Ile Thr Gly His			
	465	470	475	480
30	His Val Ser Ala Gly Ser His Ser Lys Ser Ala Phe Ser Ala Ala Thr			
	485	490	495	
	Ser His Pro Lys Pro Ile Lys Pro Ala Thr Ser His Ala Glu Pro Thr			
	500	505	510	
	Thr Ala Asp Tyr Pro Lys Pro Ala Thr Thr Ser His Pro Lys Pro Ala			
	515	520	525	
35	Ala Ala Asp Asn Pro Glu Leu Ser Ala Ser His Cys Pro Glu Ile Pro			
	530	535	540	
	Ala Ile Ala His Pro Val Ser Asp Asp Ser Asp Leu Pro Glu Ser Ala			

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545	550	555	560
Ser Ser Pro Ala Ala Gly Pro Thr Lys Pro Ala Ala Ser Gln Leu Glu			
565	570	575	
Ser Asp Thr Ile Ala Asp Leu Pro Asp Pro Thr Val Val Thr Thr Ser			
5	580	585	590
Thr Asn Asp Tyr His Asp Val Val Val Val Asp Val Glu Asp Asp Pro			
595 600 605			
Asp Glu Met Ala Val			
610			

10 (142) INFORMATION FOR SEQ ID NO:141:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1842 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:141:

ATGGGGCCCA CCCTAGCGGT TCCCACCCCC TATGGCTGTA TTGGCTGTAA GCTACCCCAG	60
CCAGAACATACC CACCGGCTCT AATCATCTTT ATGTTCTGCG CGATGGTTAT CACCATCGTT	
20 GTAGACCTAA TCGGCAACTC CATGGTCATT TTGGCTGTGA CGAAGAACAA GAAGCTCCGG	
AATTCTGGCA ACATCTTCGT GGTCAGTCTC TCTGTGGCCG ATATGCTGGT GGCCATCTAC	
240 CCATACCCCTT TGATGCTGCA TGCCATGTCC ATTGGGGGCT GGGATCTGAG CCAGTTACAG	
TGCCAGATGG TCGGGTTCATCACAGGGCTG AGTGTGGTCG GCTCCATCTT CAACATCGTG	
420 GCAATCGCTA TCAACCGTTA CTGCTACATC TGCCACAGCC TCCAGTACGA ACGGATCTTC	
25 AGTGTGCGCA ATACCTGCAT CTACCTGGTC ATCACCTGGA TCATGACCGT CCTGGCTGTC	
CTGCCAACACA TGTACATTGG CACCATCGAG TACGATCCTC GCACCTACAC CTGCATCTTC	
540 AACTATCTGA ACAACCTGT CTTCACTGTT ACCATCGTCT GCATCCACTT CGTCCTCCCT	
CTCCTCATCG TGGGTTCTG CTACGTGAGG ATCTGGACCA AAGTGCTGGC GGCCCGTGAC	
720 CCTGCAGGGC AGAATCCTGA CAACCAAATT GCTGAGGTTC GCAATAAACT AACCATGTTT	
30 GTGATCTTCC TCCTCTTGC AGTGTGCTGG TGCCCTATCA ACGTGCTCAC TGTCTGGTG	
GCTGTCAGTC CGAAGGAGAT GGCAGGCAAG ATCCCCAACT GGCTTTATCT TGCAGCCTAC	
840	

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	TTCATAGCCT ACTTCAACAG CTGCCTAAC GCTGTGATCT ACGGGCTCCT CAATGAGAAT	900
	TTCCGAAGAG AATACTGGAC CATCTTCAT GCTATGCGGC ACCCTATCAT ATTCTTCTCT	960
	GCCCTCATCA GTGATATTG TGAGATGCAG GAGGCCGTA CCCTGGCCCG CGCCC GTGCC	1020
	CATGCTCGCG ACCAAGCTCG TGAACAAGAC CGTGCCCCATG CCTGTCCCTGC TGTGGAGGAA	1080
5	ACCCCGATGA ATGTCCGGAA TGTTCCATTA CCTGGTGATG CTGCAGCTGG CCACCCCGAC	1140
	CGTGCCTCTG GCCACCCCTAA GCCCCATTCC AGATCCTCCT CTGCCTATCG CAAATCTGCC	1200
	TCTACCCACC ACAAGTCTGT CTTTAGCCAC TCCAAGGCTG CCTCTGGTCA CCTCAAGCCT	1260
	GCTCTGGCC ACTCCAAGCC TGCCTCTGGT CACCCCAAGT CTGCCACTGT CTACCCCTAAG	1320
	CCTGCCTCTG TCCATTTCAA GGCTGACTCT GTCCATTCA AGGGTGACTC TGTCCATTTC	1380
10	AAGCCTGACT CTGTTCATTT CAAGCCTGCT TCCAGCAACC CCAAGCCCCAT CACTGGCCAC	1440
	CATGTCTCTG CTGGCAGCCA CTCCAAGTCT GCCTTCAATG CTGCCACCAG CCACCCCTAAA	1500
	CCCATCAAGC CAGCTACCAG CCATGCTGAG CCCACCACTG CTGACTATCC CAAGCCTGCC	1560
	ACTACCAGCC ACCCTAAGCC CGCTGCTGCT GACAACCCTG AGCTCTCTGC CTCCCATTGC	1620
	CCCGAGATCC CTGCCATTGC CCACCCCTGTG TCTGACGACA GTGACCTCCC TGAGTCGGCC	1680
15	TCTAGCCCTG CCGCTGGGCC CACCAAGCCT GCTGCCAGCC AGCTGGAGTC TGACACCATC	1740
	GCTGACCTTC CTGACCCCTAC TGTAGTCACT ACCAGTACCA ATGATTACCA TGATGTCGTG	1800
	GTGTTGATG TTGAAGATGA TCCTGATGAA ATGGCTGTGT GA	1842

(143) INFORMATION FOR SEQ ID NO:142:

(i) SEQUENCE CHARACTERISTICS:

20	(A) LENGTH: 613 amino acids
	(B) TYPE: amino acid
	(C) STRANDEDNESS:
	(D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: protein

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:142:

	Met Gly Pro Thr Leu Ala Val Pro Thr Pro Tyr Gly Cys Ile Gly Cys	
	1 5 10 15	
	Lys Leu Pro Gln Pro Glu Tyr Pro Pro Ala Leu Ile Ile Phe Met Phe	
	20 25 30	
30	Cys Ala Met Val Ile Thr Ile Val Val Asp Leu Ile Gly Asn Ser Met	
	35 40 45	

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	Val Ile Leu Ala Val Thr Lys Asn Lys Lys Leu Arg Asn Ser Gly Asn			
	50	55	60	
	Ile Phe Val Val Ser Leu Ser Val Ala Asp Met Leu Val Ala Ile Tyr			
	65	70	75	80
5	Pro Tyr Pro Leu Met Leu His Ala Met Ser Ile Gly Gly Trp Asp Leu			
	85	90	95	
	Ser Gln Leu Gln Cys Gln Met Val Gly Phe Ile Thr Gly Leu Ser Val			
	100	105	110	
10	Val Gly Ser Ile Phe Asn Ile Val Ala Ile Ala Ile Asn Arg Tyr Cys			
	115	120	125	
	Tyr Ile Cys His Ser Leu Gln Tyr Glu Arg Ile Phe Ser Val Arg Asn			
	130	135	140	
	Thr Cys Ile Tyr Leu Val Ile Thr Trp Ile Met Thr Val Leu Ala Val			
	145	150	155	160
15	Leu Pro Asn Met Tyr Ile Gly Thr Ile Glu Tyr Asp Pro Arg Thr Tyr			
	165	170	175	
	Thr Cys Ile Phe Asn Tyr Leu Asn Asn Pro Val Phe Thr Val Thr Ile			
	180	185	190	
20	Val Cys Ile His Phe Val Leu Pro Leu Leu Ile Val Gly Phe Cys Tyr			
	195	200	205	
	Val Arg Ile Trp Thr Lys Val Leu Ala Ala Arg Asp Pro Ala Gly Gln			
	210	215	220	
	Asn Pro Asp Asn Gln Leu Ala Glu Val Arg Asn Lys Leu Thr Met Phe			
	225	230	235	240
25	Val Ile Phe Leu Leu Phe Ala Val Cys Trp Cys Pro Ile Asn Val Leu			
	245	250	255	
	Thr Val Leu Val Ala Val Ser Pro Lys Glu Met Ala Gly Lys Ile Pro			
	260	265	270	
30	Asn Trp Leu Tyr Leu Ala Ala Tyr Phe Ile Ala Tyr Phe Asn Ser Cys			
	275	280	285	
	Leu Asn Ala Val Ile Tyr Gly Leu Leu Asn Glu Asn Phe Arg Arg Glu			
	290	295	300	
	Tyr Trp Thr Ile Phe His Ala Met Arg His Pro Ile Ile Phe Phe Ser			
	305	310	315	320
35	Gly Leu Ile Ser Asp Ile Arg Glu Met Gln Glu Ala Arg Thr Leu Ala			
	325	330	335	
	Arg Ala Arg Ala His Ala Arg Asp Gln Ala Arg Glu Gln Asp Arg Ala			

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	340	345	350
	His Ala Cys Pro Ala Val Glu Glu Thr Pro Met Asn Val Arg Asn Val		
	355	360	365
5	Pro Leu Pro Gly Asp Ala Ala Ala Gly His Pro Asp Arg Ala Ser Gly		
	370	375	380
	His Pro Lys Pro His Ser Arg Ser Ser Ser Ala Tyr Arg Lys Ser Ala		
	385	390	395
	Ser Thr His His Lys Ser Val Phe Ser His Ser Lys Ala Ala Ser Gly		
	405	410	415
10	His Leu Lys Pro Val Ser Gly His Ser Lys Pro Ala Ser Gly His Pro		
	420	425	430
	Lys Ser Ala Thr Val Tyr Pro Lys Pro Ala Ser Val His Phe Lys Ala		
	435	440	445
15	Asp Ser Val His Phe Lys Gly Asp Ser Val His Phe Lys Pro Asp Ser		
	450	455	460
	Val His Phe Lys Pro Ala Ser Ser Asn Pro Lys Pro Ile Thr Gly His		
	465	470	475
	His Val Ser Ala Gly Ser His Ser Lys Ser Ala Phe Asn Ala Ala Thr		
	485	490	495
20	Ser His Pro Lys Pro Ile Lys Pro Ala Thr Ser His Ala Glu Pro Thr		
	500	505	510
	Thr Ala Asp Tyr Pro Lys Pro Ala Thr Thr Ser His Pro Lys Pro Ala		
	515	520	525
25	Ala Ala Asp Asn Pro Glu Leu Ser Ala Ser His Cys Pro Glu Ile Pro		
	530	535	540
	Ala Ile Ala His Pro Val Ser Asp Asp Ser Asp Leu Pro Glu Ser Ala		
	545	550	555
	Ser Ser Pro Ala Ala Gly Pro Thr Lys Pro Ala Ala Ser Gln Leu Glu		
	565	570	575
30	Ser Asp Thr Ile Ala Asp Leu Pro Asp Pro Thr Val Val Thr Thr Ser		
	580	585	590
	Thr Asn Asp Tyr His Asp Val Val Val Asp Val Glu Asp Asp Pro		
	595	600	605
35	Asp Glu Met Ala Val		
	610		

(144) INFORMATION FOR SEQ ID NO:143:

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- 5 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 33 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:143:

GCTGAGGTTC GCAATAACT AACCATGTTT GTG

33

(145) INFORMATION FOR SEQ ID NO:144:

- 10 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 30 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

15 (ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:144:

CTCCTTCGGT CCTCCTATCG TTGTCAGAAG T

31

(146) INFORMATION FOR SEQ ID NO:145:

- 20 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 27 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

25 (iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:145:

TTAGATATCG GGGCCCACCC TAGCGGT

33

(147) INFORMATION FOR SEQ ID NO:146:

- 30 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 29 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

- 116 -

(iv) ANTI-SENSE: YES

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:146:

GGTACCCCCA CAGCCATTTC ATCAGGATC

33



(19) World Intellectual Property Organization
International Bureau



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20 April 2000 (20.04.2000)

PCT

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(71) Applicant (for all designated States except US): ARENA PHARMACEUTICALS, INC. [US/US]; 6166 Nancy Ridge Drive, San Diego, CA 92121 (US).

(21) International Application Number: PCT/US99/24065

(72) Inventors: and

(22) International Filing Date: 13 October 1999 (13.10.1999)

(75) Inventors/Applicants (for US only): BEHAN, Dominic, P. [GB/US]; 11472 Roxboro Court, San Diego, CA 92131 (US). LEHMANN-BRUIINSMA, Karin [DE/US]; 12565 Pathos Lane, San Diego, CA 92129 (US). CHALMERS, Derek, T. [GB/US]; 347 Longden Lane, Solana Beach, CA 92150 (US). CHEN, Ruoping [CN/US]; 5296 Timber Branch Way, San Diego, CA 92130 (US). DANG, Huong, T. [US/US]; 5352 Oak Park Drive, San Diego, CA 92105 (US). GORE, Martin [GB/US]; 6868 Estrella Avenue, San Diego, CA 92120 (US). LIAW, Chen, W. [US/US]; 7668 Salix Place, San Diego, CA 92129 (US). LIN, I-Lin [—/US]; 8291-7 Gold Coast Drive, San Diego, CA 92126 (US). LOWITZ, Kevin [US/US]; Apartment C, 8031 Caminito de Pizza, San Diego, CA 92108 (US). WHITE, Carol [US/US]; 4260 Cleveland Avenue, San Diego, CA 92103 (US).

(25) Filing Language: English

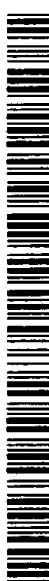
(74) Agents: MILLER, Suzanne, E. et al.; Woodcock Washburn Kurtz Mackiewicz & Norris LLP, 46th floor, One Liberty Place, Philadelphia, PA 19103 (US).

(26) Publication Language: English

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(30) Priority Data:

(84) Designated States (regional): ARIPO patent (GH, GM, KE, LS, MW, SD, SL, SZ, TZ, UG, ZW), Eurasian patent (AM, AZ, BY, KG, KZ, MD, RU, TJ, TM), European patent (AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE), OAPI patent (BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG).



A3

(63) Related by continuation (CON) or continuation-in-part (CIP) to earlier application:

US 09/170,496 (CIP)
Filed on 13 October 1998 (13.10.1998)

Published:

— With international search report.

(88) Date of publication of the international search report:
22 February 2001

For two-letter codes and other abbreviations, refer to the "Guidance Notes on Codes and Abbreviations" appearing at the beginning of each regular issue of the PCT Gazette.

WO 00/22131 A3 (54) Title: NON-ENDOGENOUS, CONSTITUTIVELY ACTIVATED HUMAN G PROTEIN-COUPLED RECEPTORS

(57) Abstract: The invention disclosed in this patent document relates to transmembrane receptors, more particularly to a human G protein-coupled receptor for which the endogenous ligand is unknown ("orphan GPCR receptors"), and most particularly to mutated (non-endogenous) versions of the human GPCRs for evidence of constitutive activity.

INTERNATIONAL SEARCH REPORT

International Application No.

PCT/US 99/24065

A. CLASSIFICATION OF SUBJECT MATTER
 IPC 7 C12N15/16 C07K14/72

According to International Patent Classification (IPC) or to both national classification and IPC

B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)
 IPC 7 C12N C07K

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practical, search terms used)

C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
A	WO 97 21731 A (NEW ENGLAND MEDICAL CENTER INC) 19 June 1997 (1997-06-19) page 18, line 16 - line 26 figures 2,3 ---	1-4
A	SCHEER A. ET AL.: "CONSTITUTIVELY ACTIVE G PROTEIN-COUPLED RECEPTORS: POTENTIAL MECHANISMS OF RECEPTOR ACTIVATION" JOURNAL OF RECEPTOR AND SIGNAL TRANSDUCTION RESEARCH, vol. 17, no. 1/03, 1997, pages 57-73, XP000867531 ISSN: 1079-9893 the whole document ---	1-4 -/-

Further documents are listed in the continuation of box C.

Patent family members are listed in annex.

* Special categories of cited documents :

- "A" document defining the general state of the art which is not considered to be of particular relevance
- "E" earlier document but published on or after the international filing date
- "L" document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified)
- "O" document referring to an oral disclosure, use, exhibition or other means
- "P" document published prior to the international filing date but later than the priority date claimed

- "T" later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention
- "X" document of particular relevance, the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone
- "Y" document of particular relevance, the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art.
- "&" document member of the same patent family

Date of the actual completion of the international search

2 March 2000

Date of mailing of the international search report

14 06 2000

Name and mailing address of the ISA

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Mandl, B

INTERNATIONAL SEARCH REPORT

Interr. Application No
PCT/US 99/24065

C.(Continuation) DOCUMENTS CONSIDERED TO BE RELEVANT

Category	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
A	WO 98 38217 A (HERRICK DAVIS KATHARINE ; TEITLER MILT (US); EGAN CHRISTINA C (US)) 3 September 1998 (1998-09-03) figure 4 ---	1-4
A	KJELLSBERG M. A. ET AL.: "CONSTITUTIVE ACTIVATION OF THE ALPHA1B-ADRENERGIC RECEPTOR BY ALL AMINO ACID SUBSTITUTIONS AT A SINGLE SITE" JOURNAL OF BIOLOGICAL CHEMISTRY, vol. 267, no. 3, 25 January 1992 (1992-01-25), pages 1430-1433, XP002911764 ISSN: 0021-9258 the whole document ---	1-4
P,A	PAUWELS P. J. ET AL.: "REVIEW:AMINO ACID DOMAINS INVOLVED IN CONSTITUTIVE ACTIVATION OF G-PROTEIN-COUPLED RECEPTORS" MOLECULAR NEUROBIOLOGY, vol. 17, no. 1/03, 1998, pages 109-135, XP000866477 ISSN: 0893-7648 the whole document ---	1-4
P,A	WO 99 24569 A (ONO PHARMACEUTICAL CO ; HAGA HISANORI (JP); NAKADE SHINJI (JP); FUK) 20 May 1999 (1999-05-20) SEQ.IDs. 1-3 -----	1-4

INTERNATIONAL SEARCH REPORT

International application No.
PCT/US 99/24065

Box I Observations where certain claims were found unsearchable (Continuation of item 1 of first sheet)

This International Search Report has not been established in respect of certain claims under Article 17(2)(a) for the following reasons:

1. Claims Nos.: because they relate to subject matter not required to be searched by this Authority, namely:

2. Claims Nos.: because they relate to parts of the International Application that do not comply with the prescribed requirements to such an extent that no meaningful International Search can be carried out, specifically:

3. Claims Nos.: because they are dependent claims and are not drafted in accordance with the second and third sentences of Rule 6 4(a).

Box II Observations where unity of invention is lacking (Continuation of item 2 of first sheet)

This International Searching Authority found multiple inventions in this international application, as follows:

1. As all required additional search fees were timely paid by the applicant, this International Search Report covers all searchable claims.

2. As all searchable claims could be searched without effort justifying an additional fee, this Authority did not invite payment of any additional fee.

3. As only some of the required additional search fees were timely paid by the applicant, this International Search Report covers only those claims for which fees were paid, specifically claims Nos.:

4. No required additional search fees were timely paid by the applicant. Consequently, this International Search Report is restricted to the invention first mentioned in the claims; it is covered by claims Nos.:

1-4

Remark on Protest

The additional search fees were accompanied by the applicant's protest.

No protest accompanied the payment of additional search fees.

FURTHER INFORMATION CONTINUED FROM PCT/ISA/ 210

1. Claims: 1-4

A cDNA encoding a non-endogenous, constitutively activated version of a human G-protein-coupled receptor comprising hARE-3(F313K); the receptor encoded by said cDNA; a plasmid comprising said cDNA; and a host cell comprising said plasmid.

2. Claims: 5-8

A cDNA encoding a non-endogenous, constitutively activated version of a human G-protein-coupled receptor comprising hARE-4(V233K); the receptor encoded by said cDNA; a plasmid comprising said cDNA; and a host cell comprising said plasmid.

3. Claims: 9-12

A cDNA encoding a non-endogenous, constitutively activated version of a human G-protein-coupled receptor comprising hARE-5(A240K); the receptor encoded by said cDNA; a plasmid comprising said cDNA; and a host cell comprising said plasmid.

4. Claims: 13-16

A cDNA encoding a non-endogenous, constitutively activated version of a human G-protein-coupled receptor comprising hGPCR14(L257K); the receptor encoded by said cDNA; a plasmid comprising said cDNA; and a host cell comprising said plasmid.

5. Claims: 17-20

A cDNA encoding a non-endogenous, constitutively activated version of a human G-protein-coupled receptor comprising hGPCR27(C283K); the receptor encoded by said cDNA; a plasmid comprising said cDNA; and a host cell comprising said plasmid.

6. Claims: 21-24

A cDNA encoding a non-endogenous, constitutively activated version of a human G-protein-coupled receptor comprising hARE-1(E232K); the receptor encoded by said cDNA; a plasmid comprising said cDNA; and a host cell comprising said plasmid.

7. Claims: 25-28

FURTHER INFORMATION CONTINUED FROM PCT/ISA/ 210

A cDNA encoding a non-endogenous, constitutively activated version of a human G-protein-coupled receptor comprising hARE-2(G285K); the receptor encoded by said cDNA; a plasmid comprising said cDNA; and a host cell comprising said plasmid.

8. Claims: 29-32

A cDNA encoding a non-endogenous, constitutively activated version of a human G-protein-coupled receptor comprising hPPR1(L239K); the receptor encoded by said cDNA; a plasmid comprising said cDNA; and a host cell comprising said plasmid.

9. Claims: 33-36

A cDNA encoding a non-endogenous, constitutively activated version of a human G-protein-coupled receptor comprising hG2A(K232A); the receptor encoded by said cDNA; a plasmid comprising said cDNA; and a host cell comprising said plasmid.

10. Claims: 37-40

A cDNA encoding a non-endogenous, constitutively activated version of a human G-protein-coupled receptor comprising hRUP3(L224K); the receptor encoded by said cDNA; a plasmid comprising said cDNA; and a host cell comprising said plasmid.

11. Claims: 41-44

A cDNA encoding a non-endogenous, constitutively activated version of a human G-protein-coupled receptor comprising hRUP5(A236K); the receptor encoded by said cDNA; a plasmid comprising said cDNA; and a host cell comprising said plasmid.

12. Claims: 45-48

A cDNA encoding a non-endogenous, constitutively activated version of a human G-protein-coupled receptor comprising hRUP6(N267K); the receptor encoded by said cDNA; a plasmid comprising said cDNA; and a host cell comprising said plasmid.

13. Claims: 49-52

FURTHER INFORMATION CONTINUED FROM PCT/ISA/ 210

A cDNA encoding a non-endogenous, constitutively activated version of a human G-protein-coupled receptor comprising hRUP7(A302K); the receptor encoded by said cDNA; a plasmid comprising said cDNA; and a host cell comprising said plasmid.

14. Claims: 53-56

A cDNA encoding a non-endogenous, constitutively activated version of a human G-protein-coupled receptor comprising hCHN4(V236K); the receptor encoded by said cDNA; a plasmid comprising said cDNA; and a host cell comprising said plasmid.

15. Claims: 57-60

A cDNA encoding a non-endogenous, constitutively activated version of a human G-protein-coupled receptor comprising hMC4(A244K); the receptor encoded by said cDNA; a plasmid comprising said cDNA; and a host cell comprising said plasmid.

16. Claims: 61-64

A cDNA encoding a non-endogenous, constitutively activated version of a human G-protein-coupled receptor comprising hCHN3(S284K); the receptor encoded by said cDNA; a plasmid comprising said cDNA; and a host cell comprising said plasmid.

17. Claims: 65-68

A cDNA encoding a non-endogenous, constitutively activated version of a human G-protein-coupled receptor comprising hCHN6(L352K); the receptor encoded by said cDNA; a plasmid comprising said cDNA; and a host cell comprising said plasmid.

18. Claims: 69-72

A cDNA encoding a non-endogenous, constitutively activated version of a human G-protein-coupled receptor comprising hCHN8(N235K); the receptor encoded by said cDNA; a plasmid comprising said cDNA; and a host cell comprising said plasmid.

19. Claims: 73-76

A cDNA encoding a non-endogenous, constitutively activated

FURTHER INFORMATION CONTINUED FROM PCT/ISA/ 210

version of a human G-protein-coupled receptor comprising hH9(F236K); the receptor encoded by said cDNA; a plasmid comprising said cDNA; and a host cell comprising said plasmid.

20. Claims: 77-80

A cDNA encoding a non-endogenous, constitutively activated version of a human G-protein-coupled AT1 receptor selected from the group consisting of hAT1(F239K), hAT1(N111A), hAT1(AT2K255IC3) and hAT1 (A243+); the receptor encoded by said cDNA; a plasmid comprising said cDNA; and a host cell comprising said plasmid.

INTERNATIONAL ARCH REPORT

Information on patent family members

Inter.	Application No.
PCT/US	99/24065

Patent document cited in search report	Publication date	Patent family member(s)		Publication date
WO 9721731	A 19-06-1997	US 5750353	A	12-05-1998
		AU 715611	B	03-02-2000
		AU 1334397	A	03-07-1997
		CA 2239293	A	19-06-1997
		EP 0869975	A	14-10-1998
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WO 9838217	A 03-09-1998	AU 6343998	A	18-09-1998
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WO 9924569	A 20-05-1999	NONE		
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